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OM nucleic - nucleic search, using sw model

Run on: August 21, 2003, 03:48:42 ; Search time 614 Seconds

(without alignments)
8137.882 Million cell updates/sec

Title: us-09-308-830A-12

Perfect score: 1851

Sequence: 1 ccatcgcgcacatcatgt.....ttagcaactatttcgtc 1851

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_19Jun03.*

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24: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
25: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1851	100.0	1851	AA51716	Streptococcus pyog
2	1851	100.0	1851	AA41593	Nucleotide sequenc
3	1835.4	99.2	1837	AA28540	S. pyogenes detect
4	1835.4	99.2	1837	ABA76857	Streptococcus pyog
5	1832.2	99.0	1837	AA251112	Streptococcal pyro
6	1832.2	99.0	1837	ABN84229	Streptococcal pyro
7	754.4	40.8	756	AAH01002	Unidentified nucle
8	184.2	10.0	1712	AA251107	Staphylococcal ent

c	9	184.2	10.0	1712	24	ABN84224	Staphylococcal ent
	10	178.8	9.7	2155561	24	ABN71527	Streptococcus poly
	11	176.2	9.5	1712	21	AA251108	Mutant Staphylococ
	12	176.2	9.5	1712	21	AA251108	Staphylococcal ent
	13	171.4	9.3	773	18	AA745698	Staphylococcus ent
	14	164.6	8.9	1095	21	AA251111	Staphylococcal ent
	15	164.6	8.9	1095	21	AA251111	Staphylococcal SEC
	16	161.2	8.7	723	21	AA245835	Mutant SEB gene en
	17	161.2	8.7	801	21	AA245834	Mutant SEB gene en
	18	161.2	8.7	1388	21	AA251109	Mutant Staphylococ
	19	161.2	8.7	1388	24	ABN84226	Staphylococcal ent
	20	159.6	8.6	867	22	AAH74983	Nucleotide sequenc
c	21	145.8	7.9	177	24	ABN66731	Streptococcus poly
c	22	126.2	7.1	186	24	ABN66706	Streptococcus poly
c	23	126.2	6.8	141	10	AA90259	Human alpha-interf
c	24	112.4	6.1	815	21	AA90259	Plant-optimized mu
c	25	107.5	5.8	180	24	ABN66707	Streptococcus poly
c	26	84.2	4.5	8056	25	AB210246	Haematopoietic cel
c	27	84	4.5	8056	25	AB210246	Haematopoietic cel
c	28	75.6	4.1	8056	25	AB210100	Haematopoietic cel
c	29	74	4.0	8056	25	AB210100	Haematopoietic cel
c	30	72.8	3.9	757	21	AA251106	Mutant Staphylococ
c	31	72.8	3.9	757	21	AA245833	Mutant SEA gene en
c	32	72.8	3.9	757	24	ABN84223	Staphylococcal ent
c	33	72.8	3.9	830	21	AA251105	Staphylococcal ent
c	34	72.8	3.9	830	24	ABN84222	Staphylococcal ent
c	35	72.8	3.9	7131	24	ABL70427	Chemically treated
c	36	72.8	3.9	7131	24	AA251106	Human gene regulat
c	37	72.8	3.9	7131	24	ABN31450	Signal transductio
c	38	71	3.8	6131	24	ABU32891	Human immune syste
c	39	70.6	3.8	626	23	ABV60941	Human prostate exp
c	40	70.4	3.8	14919	22	AA346506	Tumour suppressor
c	41	70	3.8	15548	24	ABL34155	Human immune syste
c	42	69.4	3.7	494	23	ABV10021	Human prostate exp
c	43	68.2	3.7	50000	24	ABL56202	AmEPV genome fragm
c	44	68	3.7	18683	24	ABL54334	Chemically treated
c	45	68	3.7	18683	24	ABL32313	Human immune syste

ALIGNMENTS

RESULT 1
AAT51716
ID AAT51716 standard; DNA; 1851 BP.

XX AAT51716;

AC AAT51716;

XX 04-NOV-1997 (first entry)

DE Streptococcus pyogenes Streptococcal toxin A DNA.

XX Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;
KW vaccine; protection; treatment; cancer; neutralising antibody;
KW streptococcal toxic shock syndrome; STSS; symptom; amelioration;
KW fever; hypotension; group A streptococcal infection; myositis;
KW fascitis; liver damage; T cell; lymphoma; ovarian; uterine; ss.

XX Streptococcus pyogenes.

XX Key Location/Qualifiers

FT CDS 828..1583

FT FT /*tag= a

FT sig_peptide 828..917

FT /*tag= b

FT mat_peptide 918..1580

FT /*tag= c

XX W09640930-A1.

XX 19-DEC-1996.

XX

Db 1021 TGAATCTGTGATCAACTTTTATCTCACCATTAAATATATATATGTTTCAGGGCAAAATT 1080
 QY 1081 ATGATAAATTAAGAACTGAACCTTAAGAACCAAGAGATGGCAACTTTATTATTAAGGATAAAA 1140
 Db 1081 ATGATAAATTAAGAACTGAACCTTAAGAACCAAGAGATGGCAACTTTATTATTAAGGATAAAA 1140
 QY 1141 ACCTTGATATTTATGGTGTAGAAATATTAACATCTCTCTGTTATTTATGTAAGAAATGAGAAA 1200
 Db 1141 ACCTTGATATTTATGGTGTAGAAATATTAACATCTCTCTGTTATTTATGTAAGAAATGAGAAA 1200
 QY 1201 GGAGTCATCTATCTACGGAGGGGTAACAAATCATGATGAAGGAAATCATTTAGAAATTCCTA 1260
 Db 1201 GGAGTCATCTATCTACGGAGGGGTAACAAATCATGATGAAGGAAATCATTTAGAAATTCCTA 1260
 QY 1261 AAAAGATAGTCTTAAAGTATCAATCGATGTGTATCCAAAGCCCTATCATTTGATATGTAAG 1320
 Db 1261 AAAAGATAGTCTTAAAGTATCAATCGATGTGTATCCAAAGCCCTATCATTTGATATGTAAG 1320
 Y 1321 CAATTAAGAAATGTAAGTCTCAAGAAATAGACTATAAAGTTAGAAATATCTTACAG 1380
 Db 1321 CAATTAAGAAATGTAAGTCTCAAGAAATAGACTATAAAGTTAGAAATATCTTACAG 1380
 QY 1381 ATATTAAGCAACTATATCTAATTAAGGACCTTCTAATATGAAGCTGATATATAAAGTTCA 1440
 Db 1381 ATATTAAGCAACTATATCTAATTAAGGACCTTCTAATATGAAGCTGATATATAAAGTTCA 1440
 QY 1441 TACCTAAGAAATTAAGAAAGTTTGTGTTGATTTTCCCTGAACCAAGAAATTTACTCAAT 1500
 Db 1441 TACCTAAGAAATTAAGAAAGTTTGTGTTGATTTTCCCTGAACCAAGAAATTTACTCAAT 1500
 QY 1501 CTAAATATCTTATGATATATAAAGATTAAGAAAGCTTGACTCAAAACCAAGCAAAATG 1560
 Db 1501 CTAAATATCTTATGATATATAAAGATTAAGAAAGCTTGACTCAAAACCAAGCAAAATG 1560
 QY 1561 AAGTCTACCTAACCAAGTAACTTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 1620
 Db 1561 AAGTCTACCTAACCAAGTAACTTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 1620
 QY 1621 AGAAATTTTATGCAATTTTATTAATGTAAGAAAGCTGCTATTTGATGAGCGGTTTGT 1680
 Db 1621 AGAAATTTTATGCAATTTTATTAATGTAAGAAAGCTGCTATTTGATGAGCGGTTTGT 1680
 QY 1681 TCTTATCTAAGGAGCTTTACCTCTTAATGCTGCAAAATTTTAAATGTTGGATTTTGTGA 1740
 Db 1681 TCTTATCTAAGGAGCTTTACCTCTTAATGCTGCAAAATTTTAAATGTTGGATTTTGTGA 1740
 QY 1741 TTGTCTATTTGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1800
 Db 1741 TTGTCTATTTGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1800
 QY 1801 AACACCAAAATCATAGACAGAGCTTTGTAGCTTTAGCAACTATTTTATCTGTC 1851
 Db 1801 AACACCAAAATCATAGACAGAGCTTTGTAGCTTTAGCAACTATTTTATCTGTC 1851

RESULT 3

AAT28540

ID AAT28540 standard; DNA; 1837 BP.

AC AAT28540;

XX

XX

DT 02-APR-1997 (first entry)

DE S. pyogenes detection probe #2.

XX

XX

KW Detection; probe; amplification primer; bacterial pathogen; pneumonia;

KW Escherichia coli; Klebsiella pneumoniae; Pseudomonas aeruginosa;

KW Proteus mirabilis; Streptococcus pneumoniae; Staphylococcus aureus;

KW Staphylococcus epidermidis; Enterococcus faecalis; respiratory tract;

KW Staphylococcus saprophyticus; Streptococcus pyogenes; urinary tract;

KW Haemophilus influenzae; Moraxella catarrhalis; septicaemia; meningitis;

KW infection; intra-abdominal infection; skin infection;

KW

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Query Match

Best Local Similarity 99.2%; Score 1835.4; DB 17; Length 1837;

Matches 1836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

bacterial resistance; beta-lactam antibiotic; ds.

Synthetic.

WO9608582-A2.

21-MAR-1996.

12-SEP-1995; 95WO-CA00528.

12-SEP-1994; 94US-0304732.

(BERG/) BERGERON M G.

(OUEL/) OUELLETTE M.

(ROY/) ROY P H.

Bergeron MG, Ouellette M, Roy PH;

WPI; 1996-179953/18.

Method for the detection of bacterial species using probes and

primers - allows detection and quantification of antibiotic

resistant bacteria in patients, the environment and food

Claim 57; Page 92-93; 216pp; English.

The sequences given in AAT28539-40 represent probes which were used in the method of the invention for the detection of S. pyogenes in a sample. The method comprises using probes and/or amplification primers which are specific, ubiquitous and sensitive for determining the presence and/or amount of nucleic acids from selected bacterial species in any sample, where the bacterial nucleic acid comprises a selected target region hybridisable with the probes or primers. The method comprises contacting the sample with the probes or primers and detecting the presence and/or amount of hybridised primers or amplification products as an indication of the presence and/or amount of the bacterial species. This method may be used to detect commonly encountered bacterial pathogens, e.g. Escherichia coli, Klebsiella pneumoniae, Pseudomonas aeruginosa, Proteus mirabilis, Streptococcus pneumoniae, Staphylococcus aureus, Staphylococcus epidermidis, Enterococcus faecalis, Staphylococcus saprophyticus, Streptococcus pyogenes, Haemophilus influenzae and Moraxella catarrhalis. These bacterial species are associated with approx. 90% of urinary tract infections and with a high percentage of other severe infections including septicaemia, meningitis, pneumonia, intra-abdominal infections, skin infections and other severe respiratory tract infections. The method may also be used to evaluate a bacterial resistance to beta-lactam antibiotics.

Sequence 1837 BP; 631 A; 318 C; 248 G; 640 T; 0 other;

15 TCATGTTTGACAGCTTATCATCGATAAGCTTACTTTTCGAATAGGCTCTATCTGTAAC 74

1 TCATGTTTGACAGCTTATCATCGATAAGCTTACTTTTCGAATAGGCTCTATCTGTAAC 60

75 AGGTGCAACATAGATTAGGCGATGAGATTACCAAGCAACTATGACGATATATCTAC 134

61 AGGTGCAACATAGATTAGGCGATGAGATTACCAAGCAACTATGACGATATATCTAC 120

135 ATACGCAATTCGCAATTTGATGACATTTGGAACCTAAATTCATATTTGTTACTACAAG 194

121 ATACGCAATTCGCAATTTGATGACATTTGGAACCTAAATTCATATTTGTTACTACAAG 180

195 CAACTAGATTGACACTTAATTCCTCAACAAGCTTAATTTACACACTTCAAGTACTGCC 254

181 CAACTAGATTGACACTTAATTCCTCAACAAGCTTAATTTACACACTTCAAGTACTGCC 240

255 ACCAGCTCCATCAATGCTTTACCGTAAGCTATCACTTACTATAAAGCTTTTACTACAA 314

Db 241 ACCAGTCCATCAATGCTTACCGTAAGTAATCATAACTTACTAAAAACCTTGTTACATCAA 300
QY 315 GGTGTTTTCTTTTGTCTGTTTCATGAGTTACCAATAAAGTTCTATATATTGACAACTAA 374
Db 301 GGTGTTTTCTTTTGTCTGTTTCATGAGTTACCAATAAAGTTCTATATATTGACAACTAA 360
QY 375 ATTGCAACTCTTCAATATATTTTCTGCTACTCAAAAGTTTCTTCATTTGATATAGTCT 434
Db 361 ATTGCAACTCTTCAATATATTTTCTGCTACTCAAAAGTTTCTTCATTTGATATAGTCT 420
QY 435 AATTCACCATCACTCTTCCACTCTCTACCGTCACAACTTCATCATCTCTCACTTTT 494
Db 421 AATTCACCATCACTCTTCCACTCTCTACCGTCACAACTTCATCATCTCTCACTTTT 480
QY 495 TCGTGTGTAACACATAATCAATATCTTTCCGTTTTTACGCACTATCGCTACTGTGCA 554
Db 481 TCGTGTGTAACACATAATCAATATCTTTCCGTTTTTACGCACTATCGCTACTGTGCA 540
QY 555 CCTAAATATACCCCTTATCAATCGCTCTTTTAACTCACTATATATATATATATTTT 614
Db 541 CCTAAATATACCCCTTATCAATCGCTCTTTTAACTCACTATATATATATATATTTT 600
QY 615 CCTCTACTACTATCTGTAATAAGATATAAATAAATAAATAAATAAATAAATAAATAA 674
Db 601 CCTCTACTACTATCTGTAATAAGATATAAATAAATAAATAAATAAATAAATAAATAA 660
QY 675 AATAAATAATTAATATATAGTTTAAATGTTTTTAAATAATATACAAATTTTATCTATTA 734
Db 661 AATAAATAATTAATATATAGTTTAAATGTTTTTAAATAATATACAAATTTTATCTATTA 720
QY 735 GTTACTATTTTTCATGTTAGTAATATGTTGTAATGTAATACCTTTTAAATCTAG 794
Db 721 GTTACTATTTTTCATGTTAGTAATATGTTGTAATGTAATACCTTTTAAATCTAG 780
QY 795 AGGAGAACCCAGATATAAATGAGGATATTAATGGAATAAATAAATAAATAAATAAATAA 854
Db 781 AGGAGAACCCAGATATAAATGAGGATATTAATGGAATAAATAAATAAATAAATAAATAA 840
QY 855 AAAATGGTATTTTGTGTTTGTAGTACATTTCTGGACTAACAACTCTCGCAAGAGGTATT 914
Db 841 AAAATGGTATTTTGTGTTTGTAGTACATTTCTGGACTAACAACTCTCGCAAGAGGTATT 900
QY 915 GCTCAACAAGACCCGATCCAGCCAACTTACAGATCTAGTTTGTAGTTAAATCTTCAA 974
Db 901 GCTCAACAAGACCCGATCCAGCCAACTTACAGATCTAGTTTGTAGTTAAATCTTCAA 960
QY 975 AATATATATTTTCTTTATGAGGTCACCTGTTTACTCAGGAGAAATGTAATCTGTGAT 1034
Db 961 AATATATATTTTCTTTATGAGGTCACCTGTTTACTCAGGAGAAATGTAATCTGTGAT 1020
QY 1035 CAACCTTTATCTCACCATTATATATATATATGTTTTCAGGGCCAAATATGATAAATAA 1094
Db 1021 CAACCTTTATCTCACCATTATATATATATATGTTTTCAGGGCCAAATATGATAAATAA 1080
QY 1095 ACTGAACCTTAGAACCAAGAGATGGAACCTTTATTAAGGATAAAGCTTGATATTTAT 1154
Db 1081 ACTGAACCTTAGAACCAAGAGATGGAACCTTTATTAAGGATAAAGCTTGATATTTAT 1140
QY 1155 GGTGTAGATAATATACCATCTCTGTTATTTATGTAATGCAAGAGGATGCATGTATC 1214
Db 1141 GGTGTAGATAATATACCATCTCTGTTATTTATGTAATGCAAGAGGATGCATGTATC 1200
QY 1215 TACGGAGGGTAACAAATCATGAAGGAATCATTTAGAAATTCCTAAAAAGATAGTCGTT 1274
Db 1201 TACGGAGGGTAACAAATCATGAAGGAATCATTTAGAAATTCCTAAAAAGATAGTCGTT 1260
QY 1275 AAAGTATCAATCGATGGTATCCAAAGCCCTATCATTTGATATTGAAACAAATAAAAAATG 1334
Db 1261 AAAGTATCAATCGATGGTATCCAAAGCCCTATCATTTGATATTGAAACAAATAAAAAATG 1320
QY 1335 GTAACGTCAAGAAATTAGACTATATAAGTTAGAAAAATCTTTACAGATAAATAAGCAACTA 1394
Db 1321 GTAACGTCAAGAAATTAGACTATATAAGTTAGAAAAATCTTTACAGATAAATAAGCAACTA 1380

QY 1395 TATACTAATGGACCTTCTAAATATGAACTGGATATATAAAGTTCTATACCTAAGATAA 1454
Db 1381 TATACTAATGGACCTTCTAAATATGAACTGGATATATAAAGTTCTATACCTAAGATAA 1440
QY 1455 GAAAGTTTTTGGTTGATTTTTTCCCTGAACCAAGATTTTACTCAATCTAAATATCTTATG 1514
Db 1441 GAAAGTTTTTGGTTGATTTTTTCCCTGAACCAAGATTTTACTCAATCTAAATATCTTATG 1500
QY 1515 ATATATAAGATAAATGAACGCTTGACTCAACACAAAGCCAAATTTGAAGTCTACCTAACA 1574
Db 1501 ATATATAAGATAAATGAACGCTTGACTCAACACAAAGCCAAATTTGAAGTCTACCTAACA 1560
QY 1575 ACCAAGTAACTTTTGGTTGATTTTTTGGCAACCTTACTGCTGGATTTAGAAATTTTATTC 1634
Db 1561 ACCAAGTAACTTTTGGTTGATTTTTTGGCAACCTTACTGCTGGATTTAGAAATTTTATTC 1620
QY 1635 AATCTCTTTTAAATGATAAAGCCGCTCATTTGATGAGCGGTTTTGCTTTATCTAAAGGA 1694
Db 1621 AATCTCTTTTAAATGATAAAGCCGCTCATTTGATGAGCGGTTTTGCTTTATCTAAAGGA 1680
QY 1695 GCTTTACCTCCTAAATGCTCAAAATTTTAAATGTTGATTTTGTCTTATCTTATGAT 1754
Db 1681 GCTTTACCTCCTAAATGCTCAAAATTTTAAATGTTGATTTTGTCTTATCTTATGAT 1740
QY 1755 TTGATGGGTAATCCCAATTTTTCGACAGACATCGTGGCCACCTCTAAACACCAAAATCAT 1814
Db 1741 TTGATGGGTAATCCCAATTTTTCGACAGACATCGTGGCCACCTCTAAACACCAAAATCAT 1800
QY 1815 AGACAGGAGCTGTAGCTTAGCTTAGCAACTATTTTATCGTC 1851
Db 1801 AGACAGGAGCTGTAGCTTAGCAACTATTTTATCGTC 1837

RESULT 4

AB76857
ID AB76857 standard; DNA; 1837 BP.

XX AB76857;

XX 28-JAN-2002 (first entry)

XX Streptococcus pyogenes polynucleotide SEQ ID NO 33.

XX Detection; bacterial species; animal; food; environment;
KW antibiotic resistance; ds.

XX Streptococcus pyogenes.

OS NZ501596-A.

PN 29-JUN-2001.

XX 12-SEP-1995; 95NZ-0501596.

XX 12-SEP-1995; 95NZ-0501596.

XX (IDII-) IDI INFECTIO DIAGNOSTIC INC.

XX Bergeron MG, Ouellette M, Roy PH;

XX WPI; 2001-615034/71.

XX Method for detecting target bacterial species in a sample, comprises
PT detecting the presence or amount of bacterial nucleic acid amplified by
PT a primer derived from bacterial DNA, specific for the target bacterial
PT species

PS Claim 6; Page 107-108; 168pp; English.

XX The invention relates to detecting target bacterial species suspected to
CC be present in a sample, comprising contacting nucleic acids of target
CC bacterial species with an amplification primer pair derived from a

bacterial DNA fragment (ABA76825-ABA76861) specific for the target bacterial species but ubiquitous for different strains, amplifying the nucleic acid and detecting the presence or amount of an amplified sequence as an indication of the presence or amount of the target bacterial species. The invention includes primers and probes (ABA76862-ABA76984) against the target bacterial species, especially *E. coli*, *K. pneumoniae*, *P. aeruginosa*, *P. mirabilis*, *S. pneumoniae*, *S. aureus*, *S. epidermidis*, *E. faecalis*, *S. saprophyticus*, *S. pyogenes*, *H. influenzae*, *M. catarrhalis* and/or group A *Streptococci* producing enterotoxin A gene spe A, suspected to be present in a sample which is obtained from human patients, animals, environment or food, and which consists of one or more bacterial colonies. Oligonucleotide probes and primers complementary to the bacterial genes encoding resistance to antibiotics such as bla(tem), bla(rob), bla(shv), aacDB, aacC1, aacC2, aacC3, aacA4, mecA, vanA, vanH, vanX, aacA, aac-aphD, vat, vga, msrA, sul and/or int (ABA76985-ABA77001) are also useful to identify commonly encountered and clinically important resistance genes. The invention provides a rapid method of bacterial identification that can be achieved, which reduces the time currently required for the identification of pathogens in the clinical laboratory.

Sequence 1837 BP; 631 A; 318 C; 248 G; 640 T; 0 other;

Query Match 99.28; Score 1835.4; DB 22; Length 1837;

Best Local Similarity 99.9%; Pred. No. 8.3e-286;

Matches 1836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	15	TCATGTTTGACAGCTTATCATCGATAAGCTTACTTTTCGAAATCAGGTCTATCCTTGAAAC	74
Db	1	TCATGTTTGACAGCTTATCATCGATAAGCTTACTTTTCGAAATCAGGTCTATCCTTGAAAC	60
QY	75	AGSTCGCACTAGATTAGGGCATGGAGATTTCACGACAACTATGAACGTATATACCTCAC	134
Db	61	AGSTCGCACTAGATTAGGGCATGGAGATTTCACGACAACTATGAACGTATATACCTCAC	120
QY	135	ATCAGCGCAATGGCAATTCATGACATTTGGAACTTAATTCAAATCAATTCCTTACTTAAACAAG	194
Db	121	ATCAGCGCAATGGCAATTCATGACATTTGGAACTTAATTCAAATCAATTCCTTACTTAAACAAG	180
QY	195	CAACTAGATTGCAACAATAATTCCTCAACAAAGCTTAATTTTAAACAACTATCAAGTAACCTCC	254
Db	181	CAACTAGATTGCAACAATAATTCCTCAACAAAGCTTAATTTTAAACAACTATCAAGTAACCTCC	240
QY	255	ACACGCTCCATCAATGCTTACCGTAAGCTATCATCAACTTACTTAAACCTTGTGTACATCAA	314
Db	241	ACACGCTCCATCAATGCTTACCGTAAGCTATCATCAACTTACTTAAACCTTGTGTACATCAA	300
QY	315	GGTTTTTTCTTTTGTCTGTTTCATGAGTTTACCATAACTTTCTATATTATTCGACAACTAA	374
Db	301	GGTTTTTTCTTTTGTCTGTTTCATGAGTTTACCATAACTTTCTATATTATTCGACAACTAA	360
QY	375	ATTGACAACTCTCAATTAATTTTTCTGCTCTACTCAAGGTTTTCTCATTTGATATAGCT	434
Db	361	ATTGACAACTCTCAATTAATTTTTCTGCTCTACTCAAGGTTTTCTCATTTGATATAGCT	420
QY	435	AATTCACCACTACTTCTTCCACTCTCTCTACGGTCAACAATTCATCATCTCTCACATTTT	494
Db	421	AATTCACCACTACTTCTTCCACTCTCTCTACGGTCAACAATTCATCATCTCTCACATTTT	480
QY	495	TCGTGTGGTAACACATAATCAAAATATCTTTCCGCTTTTTTACGCACTATCGCTACTGTGCA	554
Db	481	TCGTGTGGTAACACATAATCAAAATATCTTTCCGCTTTTTTACGCACTATCGCTACTGTGCA	540
QY	555	CCTAAATAATACCCCTTATCAATCGCTCTTTTAAACTCATCTATATATAACATATTTTCAT	614
Db	541	CCTAAATAATACCCCTTATCAATCGCTCTTTTAAACTCATCTATATATAACATATTTTCAT	600
QY	615	CCTCCTACCTATCTATTTCGTAAGAAAGATAAAATAAATCAACTATTTGTTTTTGTATTTTAT	674
Db	601	CCTCCTACCTATCTATTTCGTAAGAAAGATAAAATAAATCAACTATTTGTTTTTGTATTTTAT	660
QY	675	AATAAAATATTAAATATAGTTAATGTTTTTTTTTAAAAATATACAATTTATTTCTATTATTA	734

OY 1815 AGACAGAGCTGTAGCTTAGCAACTATTTATCGTC 1851
 |||||
 Db 1801 AGACAGAGCTGTAGCTTAGCAACTATTTATCGTC 1837

RESULT 5

AAZ51112
 ID AAZ51112 standard; DNA: 1837 BP.

XX AAZ51112;

XX 05-JUN-2000 (first entry)

XX Streptococcal pyrogenic exotoxin A (SPE-A) encoding DNA.

XX Superantigen toxin; SAg; Streptococcal pyrogenic exotoxin A; SPE-A;
 KW antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor;
 KW cytostatic; antibody; staphylococcal/streptococcal toxin; toxoid; SPEA42;
 KW diagnosis; treatment; superantigen-associated bacterial infection; ds.

XX Streptococcus sp.

PH Key Location/Qualifiers
 FT CDS 814..1569

FT /*tag= a

FT /product= "Streptococcal pyrogenic exotoxin A (SPE-A)"

XX W0200009154-A1.

XX 24-FEB-2000.

XX 13-AUG-1998; 98WO-US16766.

XX 13-AUG-1998; 98WO-US16766.

XX (REED-) REED ARMY INST RES WALTER.

XX Ulrich RG, Olson MA, Bavari S;

XX WPI: 2000-224177/19.

XX P-PSDB: AAY70109.

XX Nucleic acid encoding superantigen toxin useful as a vaccine and for
 PT diagnosis of superantigen-associated bacterial infections

XX Example 12; Page 92-94; 118pp; English.

XX The present sequence is the DNA encoding Streptococcal pyrogenic
 CC exotoxin A (SPE-A), a bacterial superantigen toxin (SAG), used for the
 CC formulation of SPE-A vaccine SPEA42. The coding region of this SAG toxin
 CC is altered by site directed mutagenesis, introducing L42R mutation, that
 CC results in disruption of binding of the toxin to both the MHC class II
 CC or T-cell antigen receptor. SPE-A has antibacterial and cytostatic
 CC activity. This sequence is useful for the production of SPE-A vaccines
 CC and specific antibodies. This vaccine overcomes the disadvantages of the
 CC chemically inactivated toxins and is designed to protect individuals
 CC against one or several related staphylococcal and streptococcal toxins.
 CC It is used for the diagnosis and treatment or amelioration of
 CC superantigen-associated bacterial infections.

XX Sequence 1837 BP; 632 A; 318 C; 249 G; 638 T; 0 other;

Query Match 99.08; Score 1832.2; DB 21; Length 1837;
 Best Local Similarity 99.8%; Pred. No. 2.7e-285;
 Matches 1834; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 15 TCATGTTGACAGCTTATCATCGATAAGCTTACTTTTCGAATCAGGTCTATCCTTGAAC 74

Db 1 TCATGTTGACAGCTTATCATCGATAAGCTTACTTTTCGAATCAGGTCTATCCTTGAAC 60

OY 75 AGGTGCACATAGATTAGGCGATGGAGATTACCAGACAACATGTAACGATATACATCAC 134
 |||||

Db 61 AGTGCACATAGATTAGGCGATGGAGATTACCAGACAACATGTAACGATATACATCAC 120
 OY 135 ATACGCAATCGGCAATTGATGACATTGGAATAAATTTCAATCAATTTGTTACTAACAAAG 194
 |||||
 Db 121 ATACGCAATCGGCAATTGATGACATTGGAATAAATTTCAATCAATTTGTTACTAACAAAG 180
 OY 195 CACTAGATTGACAACATAATTTCTCAACAAGGTTAATTTAAACAATTTCAAGTAACCTCC 254
 |||||
 Db 181 CACTAGATTGACAACATAATTTCTCAACAAGGTTAATTTAAACAATTTCAAGTAACCTCC 240
 OY 255 ACCAGCTCCATCAATGCTTACCGTAAGTAATCAATACTTACTAAACCTTTGTACATCAA 314
 |||||
 Db 241 ACCAGCTCCATCAATGCTTACCGTAAGTAATCAATACTTACTAAACCTTTGTACATCAA 300
 OY 315 GGTTTTTCTTTTGTCTTGTTCATGAGTTACCATAACTTTCTATATTATTATGACAACATA 374
 |||||
 Db 301 GGTTTTTCTTTTGTCTTGTTCATGAGTTACCATAACTTTCTATATTATTATGACAACATA 360
 OY 375 ATTGACAACCTCTCAATTAATTTTCTGCTACTCAAAAGTTTCTTCATTTGATATAGTCT 434
 |||||
 Db 361 ATTGACAACCTCTCAATTAATTTTCTGCTACTCAAAAGTTTCTTCATTTGATATAGTCT 420
 OY 435 AATTCCACCATCACTTCTCCACTCTCTACCGTCACAACTTCAATCTCTCACTTTT 494
 |||||
 Db 421 AATTCCACCATCACTTCTCCACTCTCTACCGTCACAACTTCAATCTCTCACTTTT 480
 OY 495 TCGTGTGTAAACACATAATCAATATCTTTCCGTTTTTACGCACTATCGCTACTGTGCA 554
 |||||
 Db 481 TCGTGTGTAAACACATAATCAATATCTTTCCGTTTTTACGCACTATCGCTACTGTGCA 540
 OY 555 CCTAAATATACCCCTTATCAATCGTCTTTTAAACTCATCTATATATAACATATTTCAT 614
 |||||
 Db 541 CCTAAATATACCCCTTATCAATCGTCTTTTAAACTCATCTATATATAACATATTTCAT 600
 OY 615 CCTCTACCTATCTATTCTGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 674
 |||||
 Db 601 CCTCTACCTATCTATTCTGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 660
 OY 675 AATAAATATTATAATTAAGTTAATGTTTTTAAATAATACAAATTTTATCTATTATA 734
 |||||
 Db 661 AATAAATATTATAATTAAGTTAATGTTTTTAAATAATACAAATTTTATCTATTATA 720
 OY 735 GTTAGCTATTTTTCATTTAGTAGTAATTAATGTTGTAATTAATTAATTAATTAATTAAT 794
 |||||
 Db 721 GTTAGCTATTTTTCATTTAGTAGTAATTAATGTTGTAATTAATTAATTAATTAATTAAT 780
 OY 795 AGGAGAACCCAGATATATAATGGAGGATATTAATGGAAACAATAAAGTAATTAAGTAAG 854
 |||||
 Db 781 AGGAGAACCCAGATATATAATGGAGGATATTAATGGAAACAATAAAGTAATTAAGTAAG 840
 OY 855 AAAATGGTATTTTGTGTTTGTGACATTTCTTGACATAACAACTCCCAAGAGGATATT 914
 |||||
 Db 841 AAAATGGTATTTTGTGTTTGTGACATTTCTTGACATAACAACTCCCAAGAGGATATT 900
 OY 915 GCTCAACAAGACCCCGATCCCAAGCACTTCCACAGATCTAGTTTAGTTTAAACCTTCAA 974
 |||||
 Db 901 GCTCAACAAGACCCCGATCCCAAGCACTTCCACAGATCTAGTTTAGTTTAAACCTTCAA 960
 OY 975 AATATATATTTTCTTTATGAGGGTGACCTGTTTACTCAGAGATGTAAGTAATGTTGAT 1034
 |||||
 Db 961 AATATATATTTTCTTTATGAGGGTGACCTGTTTACTCAGAGATGTAAGTAATGTTGAT 1020
 OY 1035 CAACCTTTATCTCACCATTAT 1094
 |||||
 Db 1021 CAACCTTTATCTCACCATTAT 1080
 OY 1095 ACTGAACCTTAAGAACCAAGAGATGCAACTTTTATTAAAGGATAAAGAGCTTGATATTTAT 1154
 |||||
 Db 1081 ACTGAACCTTAAGAACCAAGAGATGCAACTTTTATTAAAGGATAAAGAGCTTGATATTTAT 1140
 OY 1155 GGCTGAGAAATATTACCATCTCTGTTATTTATGTAAGTAATGTAAGTAATGTAAGTAAT 1214
 |||||
 Db 1141 GGCTGAGAAATATTACCATCTCTGTTATTTATGTAAGTAATGTAAGTAATGTAAGTAAT 1200

QY	555	CTTAAATATACCCCTTATCAATCGCTCTTTAAACTCATCTATATATACATATTTTCAT	614	QY	1635	AATCTCTTTTAAATTAATAAACCCTCATTTGATGAGCGGTTTTGCTTATCTAAAGGA	1694
Db	541	CTTAAATATACCCCTTATCAATCGCTCTTTAAACTCATCTATATATACATATTTTCAT	600	Db	1621	AATCTCTTTTAAATTAATAAACCCTCATTTGATGAGCGGTTTTGCTTATCTAAAGGA	1680
QY	615	CTCTACCTATCTATTCGTAAAGAGATAAAATAACTATTTGTTTTTTGTTATTTAT	674	QY	1695	GCTTTACCTCCCTAAATGCTGCAAAATTTTAAATGTTGGATTTTGTATTTGTCATTGTAT	1754
Db	601	CTCTACCTATCTATTCGTAAAGAGATAAAATAACTATTTGTTTTTTGTTATTTAT	660	Db	1681	GCTTTACCTCCCTAAATGCTGCAAAATTTTAAATGTTGGATTTTGTATTTGTCATTGTAT	1740
QY	675	ATAAAATTAATAATAGTTAAATGTTTTTAAATAATATACAAATTTTATCTATTATTA	734	QY	1755	TTGATCGGTAAATCCCATTTTTCGACAGACATCGTCTGCACCTCTAACACCAAAATCAT	1814
Db	661	ATAAAATTAATAATAGTTAAATGTTTTTAAATAATATACAAATTTTATCTATTATTA	720	Db	1741	TTGATCGGTAAATCCCATTTTTCGACAGACATCGTCTGCACCTCTAACACCAAAATCAT	1800
QY	735	GTTAGCTATTTTTCATTTAGTAAATTTGGTGAATTTGTAATAACCTTTTAAATCTAG	794	QY	1815	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1851
Db	721	GTTAGCTATTTTTCATTTAGTAAATTTGGTGAATTTGTAATAACCTTTTAAATCTAG	780	Db	1801	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1837
QY	795	AGAGAACCCAGATATAAATGAGGAATTAATGGAACAAATATAAAGATTAATGAAG	854	QY	1815	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1851
Db	781	AGAGAACCCAGATATAAATGAGGAATTAATGGAACAAATATAAAGATTAATGAAG	840	Db	1801	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1837
QY	855	AAATGCTATTTTCTTTTGTAGTACATTTCTTGGACTAACATCTCGCAAGAGGTATT	914	QY	1815	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1851
Db	841	AAATGCTATTTTCTTTTGTAGTACATTTCTTGGACTAACATCTCGCAAGAGGTATT	900	Db	1801	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1837
QY	915	GCTCAACAGACCCGATCCAGCCCACTTCACAGATCTAGTTTAGTTTAAACCTTCAA	974	QY	1815	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1851
Db	901	GCTCAACAGACCCGATCCAGCCCACTTCACAGATCTAGTTTAGTTTAAACCTTCAA	960	Db	1801	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1837
QY	975	ATATATATTTTCTTTATGAGGTGACCCCTGTTACTACAGAGAAATGTGTTGAT	1034	QY	1815	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1851
Db	961	ATATATATTTTCTTTATGAGGTGACCCCTGTTACTACAGAGAAATGTGTTGAT	1020	Db	1801	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1837
QY	1035	CAACTTTTATCTCACCATTATATATATATGTTTTCAGGGCCAAATATGATAAATAA	1094	QY	1815	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1851
Db	1021	CAACTTTTATCTCACCATTATATATATATGTTTTCAGGGCCAAATATGATAAATAA	1080	Db	1801	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1837
QY	1095	ACTGAACCTTAAGAACCAAGAGATGGCAACTTTATTTAAGGATAAATAACCTTAT	1154	QY	1815	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1851
Db	1081	ACTGAACCTTAAGAACCAAGAGATGGCAACTTTATTTAAGGATAAATAACCTTAT	1140	Db	1801	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1837
QY	1155	GGTGTAGATATTTACCATCTCTGTTATTTATGTAAGAAATGCAGAAAGGATGATGTC	1214	QY	1815	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1851
Db	1141	GGTGTAGATATTTACCATCTCTGTTATTTATGTAAGAAATGCAGAAAGGATGATGTC	1200	Db	1801	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1837
QY	1215	TACGGAGGGTAAACAATCATGAAGGAATCATTTAGAAATTCCTTAAAGATAGTCGTT	1274	QY	1815	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1851
Db	1201	TACGGAGGGTAAACAATCATGAAGGAATCATTTAGAAATTCCTTAAAGATAGTCGTT	1260	Db	1801	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1837
QY	1275	AAAGTATCAATCGATGGTATCCAAAGCCCTATCATTTTGATATTTGAAACAAATAA	1334	QY	1815	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1851
Db	1261	AAAGTATCAATCGATGGTATCCAAAGCCCTATCATTTTGATATTTGAAACAAATAA	1320	Db	1801	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1837
QY	1335	GTAACCTGCTCAAGAAATAGACTATAAAGTTAGAAATATCTTACAGATATAAGCACTA	1394	QY	1815	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1851
Db	1321	GTAACCTGCTCAAGAAATAGACTATAAAGTTAGAAATATCTTACAGATATAAGCACTA	1380	Db	1801	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1837
QY	1395	TATACTAATGGACCTTCTAAATATGAACCTGGATATATAAGTTTCATACCTAAGATAA	1454	QY	1815	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1851
Db	1381	TATACTAATGGACCTTCTAAATATGAACCTGGATATATAAGTTTCATACCTAAGATAA	1440	Db	1801	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1837
QY	1455	GAAAGTTTTTGGTTGATTTTTTCCCTGAACCAAGAAATTTACTCAATCTAAATCTTATG	1514	QY	1815	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1851
Db	1441	GAAAGTTTTTGGTTGATTTTTTCCCTGAACCAAGAAATTTACTCAATCTAAATCTTATG	1500	Db	1801	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1837
QY	1515	ATATATAAGATTAATGAAGCTTTGACTCAACAGCAAGCAAAATGAAGTCTACCTAACA	1574	QY	1815	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1851
Db	1501	ATATATAAGATTAATGAAGCTTTGACTCAACAGCAAGCAAAATGAAGTCTACCTAACA	1560	Db	1801	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1837
QY	1575	ACCAAGTAACCTTTTCTTTGCGCAACCTTACCTACTGCTGGATTTAGAAATTTATGTC	1634	QY	1815	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1851
Db	1561	ACCAAGTAACCTTTTCTTTGCGCAACCTTACCTACTGCTGGATTTAGAAATTTATGTC	1620	Db	1801	AGACAGAGCTGCTAGCTTAGCAACTATTTTATCGTC	1837

RESULT 7
AAH01002

ID AAH01002 standard; DNA; 756 BP.

XX AAH01002;

XX 24-JUL-2001 (first entry)

XX Unidentified nucleotide sequence SEQ ID NO:993.

Species specific; genus specific; family specific; probe: detection;
Identification; algal; archaeal; bacterial; fungal; parasitological;
microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial;
KW vaccine; primer; ds.

XX Unidentified.

XX WO200123604-A2.

XX 05-APR-2001.

XX 28-SEP-2000; 2000WO-CA01150.

XX 28-SEP-1999; 99CA-2283458.

XX 19-MAY-2000; 2000CA-2307010.

XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.

XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;

XX Picard FU, Roy PH;

XX WPI; 2001-245006/25.

Nucleic acid sequences are used to generate universal probes and
primers which can be used to identify and detect the presence of algal,
archaeal, bacterial, fungal and parasitological species in a test sample -
Disclosure; Page 957; 1580pp; English.

The present invention describes a method for generating a repertory of
nucleic acids of tuf, fus, acpD and/or recA genes from which probes
and/or primers are derived. The method comprises amplifying the nucleic
acids of determined algal, archaeal, bacterial, fungal and parasitological
species with a combination of defined primer pairs. The method can be
used for producing probes and/or primers for detecting one or more
related microorganisms e.g. algae, archaea, bacteria, fungi and
parasites, for universal detection and for specific and ubiquitous
detection and identification of an algal, archaeal, bacterial, fungal
and parasitological species, genus, family and group. A nucleic acid (I)
obtained using the method of the invention can be used for the universal
detection of any bacterium, fungus or parasite in a sample and for the
detection of at least one antimicrobial agent resistance gene or at
least one toxin gene. hexA nucleic acids are used for the specific and
ubiquitous detection and for identification of Streptococcus pneumoniae.

KW	Enterotoxin B; superantigen; antigen; toxin; vaccine; B42360210;
XX	attenuation; mutant; gene; ss.
XX	Staphylococcus sp.
XX	
XX	Key Location/Qualifiers
PH	244..1044
FT	/*tag= a
FT	/product= "SEB vaccine"
FT	
XX	
XX	US6399332-B1.
PN	
XX	
XX	04-JUN-2002.
PD	
XX	
XX	01-SEP-1998; 98US-0144776.
PF	
XX	
XX	25-JUN-1997; 97US-0882431.
PR	
XX	
XX	(USSA) US SEC OF ARMY.
FA	
XX	
XX	Ulrich RG, Olson MA, Bavari S;
PI	
XX	
XX	WPI: 2002-546281/58.
DR	
DR	P-PSDB; ABB79503.
XX	
XX	Novel isolated and purified superantigen toxin DNA fragment which has
PT	been genetically altered, useful for producing vaccine for treatment of
PT	superantigen toxin-associated bacterial diseases
XX	
XX	Disclosure; Column 39-41; 46pp; English.
PS	
XX	
CC	The present sequence is the coding sequence of staphylococcal
CC	enterotoxin B (SEB) vaccine B42360210. The invention relates to a
CC	vaccine against superantigen toxin-associated bacterial diseases.
CC	Superantigen vaccines were developed by engineering changes in the
CC	receptor-binding portions of superantigen toxins such as SEB to
CC	reduce receptor-binding affinities and toxicity while maintaining
CC	antigenicity. In examples from the invention, attenuated
CC	superantigen toxins were shown to protect animals against challenge
CC	with wild-type toxin. Methods of producing and using the altered
CC	superantigen toxins as vaccines, and in diagnosis and therapy, are
CC	provided. A multivalent vaccine consisting of altered superantigen
CC	toxins from SEA, SEB, SEC-1, TSSP-1 and streptococcal SPEA is
CC	predicted to provide protective immunity against the majority of
CC	bacterial superantigen toxins.
XX	
XX	Sequence 1712 BP; 596 A; 223 C; 255 G; 638 T; 0 other;
SQ	
Query Match 10.0%; Score 184.2; DB 24; Length 1712;	
Best Local Similarity 54.5%; Pred. No. 6.3e-21;	
Matches 552; Conservative 0; Mismatches 408; Indels 53; Gaps	
Qy	621 ACCTATCTATTCGTAAGAAGTAAATACTATGTTTTTTTGGTTATTTAATAAAA
Db	
Qy	29 AACACTATGTTGTTAAAGAGTTCCTCGTATATAAGTTTAGGTGATGATAGTTACTTAAT
Db	
Qy	681 ATTATTAATATAAGTTTAATGTTTTTTTAAAAATATACAAATTTATCTCTATTTATAGTAGTC
Db	
Qy	89 TTTAAAGCATACTTAATTAATATAATAACATACAGATTATTAATAATTAAGTTTC
Db	
Qy	741 TATTTTTTCATGTTAGTAATATGTTGGAATGTTAAACCTTTTTAAATCTAGAGGAGA
Db	
Qy	149 TTTTAATGTTTTTTTTTAAATGGAATTTAAAGATTATAACATATATTTAAAGTGATCTAGA
Db	
Qy	801 ACCAGATATAAA--ATGGAGGATATATTAATGGAAACAATAAAAAAGTATTGAAGAAA
Db	
Qy	209 TACTTTTTTGGGAATGTTGGATAAAGGAGATAAAAAATGTAAGAGATTATTTATTTTCAC
Db	
Qy	859 TGGTATTTTTTGTTTTT--AGTGACATTTCTTTGGACTAACCAATCTCCAGAGAGTATTG
Db	
Qy	269 ATGTAATTTTGATTAATTCGACTGATATAGTTATTTCTACACCAACGTTTTAGCAGAGA
Db	
Qy	916 CTCACAAGACCCCGATCCAGCCAACCTTCACAGATCTAGTTTATGTTAA---AAACCTTC
Db	

916 CTCAACAAGACCCGGATCCAGGCACCTTCACAGATCTAGTTTAGTTAA --- AACCTTC 972
Ov

XX Superantigen toxin; Sag; Staphylococcal enterotoxin B; SEB; cytostatic;
 KW antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor;
 KW antibody; toxoid; staphylococcal/streptococcal toxin; diagnosis; mutant;
 KW treatment; superantigen-associated bacterial infection; B2360210P; ds.
 XX Staphylococcus sp.

Key Location/Qualifiers
 CDS 244..1044
 /tag= a
 /product= "Mutant Staphylococcal enterotoxin B"
 247..327
 sig_peptide
 /tag= b
 328..1041
 mat_peptide
 /tag= c
 /label= Mature_Staphylococcal_enterotoxin_B
 /note= "Mutant sequence inclusive of ATG start codon".
 /transl_except= (pos:502..504, aa:Asp)
 /transl_except= (pos:772..774, aa:Tyr)
 /transl_except= (pos:901..903, aa:Gln)
 /transl_except= (pos:904..909, aa:Asn)
 /transl_except= (pos:1012..1014, aa:Leu)

WO200009154-A1.

24-FEB-2000.

13-AUG-1998; 98WO-US16766.

13-AUG-1998; 98WO-US16766.

(REED-) REED ARMY INST RES WALTER.

Ulrich RG, Olson MA, Bavari S;

WPI; 2000-224177/19.

P-PSDB; AAY70105.

Nucleic acid encoding superantigen toxin useful as a vaccine and for
 diagnosis of superantigen-associated bacterial infections

Claim 5; Page 79-81; 118pp; English.

The present sequence is the DNA encoding mutant Staphylococcal
 enterotoxin B (SEB), a bacterial superantigen toxin (Sag), used for the
 formulation of SEB vaccine B2360210P. The coding region of this Sag
 toxin is altered by site directed mutagenesis, that results in disruption
 of binding of the toxin to both the MHC class II or T-cell antigen
 receptor. SEB has antibacterial and cytostatic activity. This sequence is
 useful for the production of SEB vaccines and specific antibodies. This
 vaccine overcomes the disadvantages of the chemically inactivated toxoids
 and is designed to protect individuals against one or several related
 staphylococcal and streptococcal toxins. It is used for the diagnosis
 and treatment or amelioration of superantigen-associated bacterial
 infections.

Sequence 1712 BP; 597 A; 224 C; 256 G; 635 T; 0 other;

Query Match 9.5%; Score 176.2; DB 21; Length 1712;
 Best Local Similarity 54.0%; Pred. No. 1.2e-19;
 Matches 547; Conservative 0; Mismatches 413; Indels 53; Gaps 7;

QY 621 ACCTATCTATTCGTAAGAAGTAAATAAATAACTATGTTTTTTTGGTTATTTATAATAAA 680
 Db 29 AACACTATGTTGTAAGAAGTATTCGTATATAGTTTAGGTGATGATAGTACTTAAT 88
 QY 681 ATTATTAATAAGTAAATGTTTTTAAAAATATACAAATTTATCTATTTATAGTTAGC 740
 Db 89 TTTAAAGCATACCTTAATTAATAATAACATGAGATTAATTAATAATAATTAAGTTTC 148
 QY 741 TATTTTTCATGTTAGTAAATATGGTGAATGTTAAATACCTTTTAAATCTAGAGAGA 800

Db 149 TTTTAATGTTTTTTTAAATGAATATTTAAGATTATAACATATATTTAAAGTGTATCAGA 208
 QY 801 ACCCAGATATAAA--ATGGAGGATATATTAATGGAAACAATAAAAAGTATTGAAGAAA 858
 Db 209 TACTTTTTGGGAATGTTGGATATAAGAGATAAAAAATGATATGAAGAGATTATTTATTCAC 268
 QY 859 TGGTATTTTTTTGTTTT---AGTGACATTTCTTGGACTAAACAATCTCGCAAGAGGTATTG 915
 Db 269 ATGTAATTTTGATATTCGCACCTGATATTATTCTACACCCCAACGTTTACGAGAGA 328
 QY 916 CTCACAAGACCCCGATCCCAAGCAACTTCACAGACTAGTTTATGTTAA---AAACCTTC 972
 Db 329 GTCAACCAAGTCCCTAAACCAAGATGAGTTGCACAATCGATTAATTCCTGCTGTTGAGG 388
 QY 973 AAAATATATATTTTCTTTATGAGGGTGACCCGTTTACTCACGAGAATGTGAAATCTGTTG 1032
 Db 389 AAAATATGAAGTTTTTGTATGATGATTAATCAATGATCAGCAATAAACGTTAAATCTATAG 448
 QY 1033 ATCAACTTTTATCTCACCATTTAATATATATATGTTTTCAGGGCCA-----AATTATG 1083
 Db 449 ATCAATTTTCGATACCTTTTGACTTAATATATCTTATTAAGGACACATAAGTTAGGGAATTATG 508
 QY 1084 ATAAATTAATACTGAACCTTAAGAACAAGAGATGGCAACTTTATTTAAGATATAAAGC 1143
 Db 509 ATATGTTTCGAGTCGAATTTAAAAACAAGATTTAGCTGATATAATACAAAGATAAATACG 568
 QY 1144 TTGATATTTATGGTGTAGAATATTACCATCTCTGTTATTTATGTAATA-----1192
 Db 569 TAGATGTTTGGAGCTAATGCTTATTTATCAATGTGCTTTTCTAAAAAAGCAATGATG 628
 QY 1193 -----TCGAGAAAGAGTGCATGTATCTACGGAGGGGTAAACAATCATG 1236
 Db 629 TTAATTCGCATCAAACTGACAAACGAAAAAATCTGTATGTTGTTGTTAACTGAGCATA 688
 QY 1237 AAGGAATCATTTAGAAATTCCTAAAAGATAGTCGTTTAAAGTATCAATCGATGTTATCC 1296
 Db 689 ATGGAACCAATTTAGATAAATATAGAAGTATTACTGTTGCGGTATTTGAAGATGGTAAAA 748
 QY 1297 AAAGCCATCATTTTATGATTTGAAACAATAAAAAATGTTAACTGCTCAAGAATTAGACT 1356
 Db 749 ATTTATTTATCTTTTGACGTACAACTAATAAGAAAAAGGTGCTGCTCAAGNATTAGATT 808
 QY 1357 ATAAAGTTAGAAAAATATCTTTACAGATAATAAGCAACTATATACATAATGAGCCTTCTAAAT 1416
 Db 809 ACCTAATCTGTCACATATTGTTGTAATAAATAAAAAAATCTATGAATTTTAAACAACCTG 868
 QY 1417 ATGAACTGGATATATAAAGTTTCATACCTAAGATAAAGAAAGTTTTTGGTTGATTTTT 1476
 Db 869 ATGAAACGGGATATATAAATTTATA---GAAAATGAGANTAGCTTTTGGTATGACATGA 925
 QY 1477 TCCCTGAACCCAG-----AATTTACTCAATCTAAATATCTTATGATATATAAAGATAATG 1530
 Db 926 TGCCTGCACCGAGAGATAAATTTGCCAANTCTAATATTAAATGATGATACATGACATA 985
 QY 1531 AAACGCTGTGACTCAACACCAAGCCAAATTTGAAGTCTACCTAACCAACCAAGTAA 1583
 Db 986 AATGGTTGATTTCTAAAGATGTAAGATTGAAGTTTATCTTACGACAAAGAAA 1038

RESULT 12
 ABN84225
 ID ABN84225 standard; cDNA; 1712 BP.

XX AC ABN84225;

XX DT 23-SEP-2002 (first entry)

XX Staphylococcal enterotoxin B vaccine, periplasmic (B899445P).

XX Enterotoxin B; superantigen; antigen; toxin; vaccine; B899445P;

XX attenuation; mutant; gene; ss.

OS Staphylococcus sp.

OS Synthetic.

Key Location/Qualifiers
CDS 244..1044
/tag- a
/product= SEB vaccine, periplasmic"
/transl_except= (pos:772..774,aa:Tyr)
244..327
sig_peptide /tag- b
mat_peptide 328..1041
/tag- c

US6399332-B1.

04-JUN-2002.

01-SEP-1998; 98US-0144776.

25-JUN-1997; 97US-0882431.

(USSA) US SEC OF ARMY.

Ulrich RG, Olson MA, Bavari S;

WPI; 2002-546281/58.

P-PSDB; ABB79504.

Novel isolated and purified superantigen toxin DNA fragment which has been genetically altered, useful for producing vaccine for treatment of superantigen toxin-associated bacterial diseases

Disclosure; Column 43-46; 46pp; English.

The present sequence is the coding sequence of staphylococcal enterotoxin B (SEB) vaccine, periplasmic (A489270P). The vaccine comprises 3 amino acid substitutions introduced into the SEB sequence: Y89A, Y94A and L45R. These mutations reduce the binding of the toxin to major histocompatibility complex (MHC) Class II and/or T cell receptors. The present DNA sequence is useful in the production of the vaccine. The full-length expressed product is secreted into the periplasmic space of *Escherichia coli* host cells, and the leader peptide is recognised and cleaved by a native mechanism. The vaccine is used to protect against superantigen toxin infections. Superantigen attributes are absent, but the superantigen is effectively recognised by the immune system and an appropriate antibody response is produced. In examples from the invention, attenuated superantigen toxins were shown to protect animals against challenge with wild-type toxin. Methods of producing and using the altered superantigen toxins as vaccines, and in diagnosis and therapy, are provided. A multivalent vaccine consisting of altered superantigen toxins from SEA, SEB, SEC-1, TSST-1 and streptococcal SPEa is predicted to provide protective immunity against the majority of bacterial superantigen toxins.

Sequence 1712 BP; 597 A; 224 C; 256 G; 635 T; 0 other;

Query Match 9.5%; Score 176.2; DB 24; Length 1712;
Best Local Similarity 54.0%; Pred. NO. 1.2e-19;
Matches 547; Conservative 0; Mismatches 413; Indels 53; Gaps 7;
QY 621 ACCATCTATCTGTAAGAGATAAAATAACATATGTTTTTTTGTATTTTATATAATAA 680
DB 29 AACACATGTTGTTAAAGATGTTTCGATATAAAGTTAGGTGATGATAGTACTTAAT 88
QY 681 ATTATATATATAAGTTAATGTTTTTAAATAATACAAATTTATCTATTTATAGTTAGC 740
DB 89 TTTAAAGCATAACCTAATTAATATAATAAATAACAGATTAATAATAATTAAGTTTC 148
QY 741 TATTTTTCATGTTAGTAATATGTTGAATTTGTAATACCTTTTAAATCTAGAGGAGA 800
DB 149 TTTTAAATGTTTTTTTAAATTAAGATTAATAACATATATTTAAAGTGATCTAGA 208

QY 801 ACCCAGATATAAA--ATGAGAGAAATATTAAATGGAACAAATAAAAGATTTATTGAAGAA
DB 209 TACTTTTTTGGGAATCTGGATAAAGAGAGATAAAAAATGTATTAAGAGATTTATTATTCTC
QY 859 TGGTATTTTTTGTGTTTT--AGTGACATTTCTTGGGACTAACAATCTCGCAAGAGGATTT
DB 269 ATGTAATTTTGTATATTCGCACCTGATATTAGTTATTCTACACCAACGCTTTTAGCAGAG
QY 916 CTCACAAGACGCCGATCCAAGCCAACCTTCACAGATCTAGTTTGTAGTTAA--AAACCTT
DB 329 GTCACACAGATCCTTAACCCAGATGAGTTGCCACAATCGAGTAATCTACTGTTTGTGAT
QY 973 AAAATATATATTTTCTTTATGAGGGTGACCCCTGTCTACTCACAGAGATGTGAATCTGTT
DB 389 AAAATATGAAGCTTTTGTATGATGATATCATGTATCAGCAATAAACGTTAAATCTATAT
QY 1033 ATCAACTTTTATCTCACCATTAAATATATATAATGTTTTCAGGGCCA-----AATTAT
DB 449 ATCAATTTTCGATACTTTGACTTTAAATATATTTCTTAAGGACACTAAGTTAGGGAATTA
QY 1084 ATAAATTAATAACTGAACCTTAAGAACCAAGAGATGGCAACTTTATTTAAGGATAAAAAA
DB 509 ATAATGTTTCGAGTCGAATTTAAACACAAGATTTAGCTGATAACACAAGATAAATA
QY 1144 TTGATATTTTANGGTGTAGAAATATTACCACTCTCTGTTATTTATGTGAAAA-----
DB 569 TAGATGTGTTGGAGCTAATGCTTATATCAATATGCTTTTCTTAAAAAAGCAATGAT
QY 1193 -----TGCAGAAAGGAGTGCATGTATCTACGAGGGGTAAACAATCAAA
DB 629 TTAATTCGCATCAAACTGACAAACGAAAAAATCTGTATGTATGTTGTTGTAACCTGAGCA
QY 1237 AAGGGAATCATTTAGAAATTCCTAAAGAGATAGTCTGTTAAAGTATCAATCGATGTTAT
DB 689 ATGGAACCAATTAGATAATATAGNAGTATTACTGTCGGGTATTTGGAAGATGGTA
QY 1297 AAGGCTATCATTTGATTTGAACAATAATAAATAATGTTAATGCTGCTCAAGAAATTAGA
DB 749 ATTTATTTATTTTGTGACGTACAAACTTAATAAGAAAAAGGTGACTGCTCAAGAAATTAGA
QY 1357 ATAAAGTTAGAAATATCTTACAGATAATAAGCAACTATATATCTAATGACCTTCTTAA
DB 809 ACCTAACCTGCTCATTATTTGGTGAATAATAAATAAATACTCTATGAATTAACAACCTGCT
QY 1417 ATGAAACTGGATATATAAAGTTTCATACCTTAAGAAATAAAGAAAGTTTTTGTGTTGATTT
DB 869 ATGAAACGGATATATTAAATTTATA--GAAATGAGATAGCTTTTGGTATGACAT
QY 1477 TCCCTGAACCCAG-----AATTTACTCAATCTAAATATCTTATGATATATAAAGATAAT
DB 926 TGCCTGCACCGAGAGATAAATTTGACCAATCTAAATATTTAATGATGTACAATGACA
QY 1531 AAACGCTTGACTCAACACACACCAAAATTTGAAGTCTTACCTACACACCAAGTAA 1583
DB 986 AAATGTTGATTTCTAAAGATGTGAAGATTTGAAGTTTATCTTACGACAAAGAAA 1038

RESULT 13
AAT45698
ID AAT45698 standard; cDNA; 773 BP.
XX
AC AAT45698;
XX
DT 08-MAR-1997 (first entry)
XX
DE Staphylococcus enterotoxin B cDNA.
XX
KW Enterotoxin B; SEB; superantigen; antigen; cytokine; chemokine;
KW T cell; lymphocyte; monocyte; natural killer cell; gene therapy;
XX cancer; vaccine; adjuvant; ss.
OS Staphylococcus sp.
XX


```
Db      323  ATAAATTTAGGGCACATGATTTTAAATTTATAACATTTAGTGATAAAAACTGAAAAATTTATG 382
Qy      1084  ATAAATTTAAACACTGAACCTTAAGAACCAAGAGATGGCAACTTTATTAAAGGATAAAAAACG 1143
Db      383  ACAAGTCAAAACAGAGTTATTAAAGAGGTTTAGCAAGAGTTAGCAAGAGTACAAAGATGAAGTAG 442
Qy      1144  TTGATATTTATGGTGTAGAATATTACCATCTCTGTTATTAT----- 1185
Db      443  TTGATGTGTATGGATCAATTAATCTATGTAAACTGCTATTTTCATCCAAAGATAATGTAG 502
Qy      1186  GTGAAATGAGAAAGAGTGCATGTATCTACGGAGGGTAACAAATCATCAGGGGAATC 1245
Db      503  GTAAAGTTACAGTGGCAAACTTGATGTATGGAGGATAACAAAAACATCAAGGAAACC 562
Qy      1246  ATTTAGAAATTCCTA-----AAAAGATACCTCGTTAAAGTATCAATCGATGGTATCCAAA 1299
Db      563  ACTTTGATAATGGGAACCTTACAAATGTACTTTATAGAGTTTATGAAAAATAAAGAAACA 622
Qy      1300  GCCTATCATTTGATATTGAACAAATAAAAAAATGGTAACTGCTCAAGAAATTAGACTATA 1359
b      623  CAATTTCTTTTGAAGTGCACACTGATAAGAAAGTGTAAACAGCTCAGAACTAGACATAA 682
Qy      1360  AAGTTAGAAATATCTTACAGATAAAGCAACTATATACTAATATGGACCTTCTAAATATG 1419
Db      683  AAGCTAGGAATTTTAAATTAATAAAAAAATTTGTATGAGTTTAAACAGTTTACCATATG 742
Qy      1420  AAAGTGAATATAAAGTTTCATACCTTAAGATAAAGAAAGTTTTGGTTTGATTTTTC 1479
Db      743  AAACAGGATATATAAATTTATTGAAATTAACGGCAATCTTTTGGTATGATATGATGC 802
Qy      1480  CTGAACCGAG-----AATTTACTCAATCTAAATATCTTATGATATATAAAGATAATGAAA 1533
Db      803  CTGACACCGCGATAAGTTTGACCAATCTAAATATTAAATGATGTACACGACAATAAAA 862
Qy      1534  CGCTTGACTCAACACACAGCCAAATTGAAGTCTACCTTAACCAACAGTA 1582
Db      863  CGGTTGATTTCTAAAGTGTGAAGATAGAGTCCACCTTACACCAAGAA 911
```

Search completed: August 21, 2003, 06:35:13
Job time : 625 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 21, 2003, 12:20:34 ; Search time 36 Seconds
(without alignments)
670.509 Million cell updates/sec

Title: US-09-308-830A-13

Perfect score: 1323

Sequence: 1 MNNKKVLKMKWFVFLVTF.....KDNETLDSNTSQIEVYLTTK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1314	99.3	251	1	S29659
2	1238	93.6	236	2	S18783
3	1233	93.2	236	2	S18786
4	1108	83.7	236	2	S18789
5	1074.5	81.2	250	1	A26152
6	575.5	43.5	266	1	ENSAB6
7	550.5	41.6	266	2	S11885
8	548	41.4	266	2	A60114
9	547	41.3	266	1	ENSAC1
10	480	36.3	258	2	G89968
11	345	25.8	260	2	A33953
12	341	25.8	260	2	C89984
13	337	25.5	136	2	A89969
14	337	25.5	260	2	E89969
15	316.5	23.9	258	2	H89968
16	313	23.7	257	2	A28179
17	312	23.6	257	2	A28864
18	304.5	23.0	240	2	G89991
19	270	20.4	239	2	D89969
20	245.5	18.6	242	2	C89969
21	210	15.9	235	2	A30809
22	173	13.1	133	2	B89969
23	129.5	9.8	231	2	D89907
24	127	9.6	157	2	A89942
25	125	9.4	227	2	C89808
26	118	8.9	234	2	C89992
27	117.5	8.9	234	2	C89807
28	116	8.8	234	1	XCSAS1
29	114	8.6	232	1	B89807

30 112 8.5 232 2 F89807
31 110.5 8.4 231 2 H89806
32 109.5 8.3 1367 2 T18466
33 106.5 8.0 241 2 B89888
34 106 8.0 434 2 T28342
35 105.5 8.0 596 2 E96935
36 105.5 8.0 825 2 H82885
37 104.5 7.9 241 2 C89888
38 103.5 7.8 1306 2 T28313
39 103.5 7.8 1856 2 C95008
40 103 7.8 235 2 C97252
41 102.5 7.7 768 2 D71726
42 102.5 7.7 1790 2 S67593
43 101.5 7.7 518 2 G70174
44 101 7.6 387 2 E82881
45 101 7.6 770 2 B48910

ALIGNMENTS

RESULT 1

S29659

exotoxin type A precursor (allele 1) - Streptococcus pyogenes phage T12

N:Alternate names: erythrogenic toxin; scarlet fever toxin

C:Species: Streptococcus pyogenes phage T12

C:Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 10-Sep-1999

C:Accession: S29659; S18782; S18784; S18785; S18791; S18796; S18797; S18800

R:Weeks, C.R.; Ferretti, J.J.

Infect. Immun. 52, 144-150, 1986

A:Title: Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin

A:Reference number: S29659; MUID:86166804; PMID:3514452

A:Accession: S29659

A:Molecule type: DNA

A:Residues: 1-251 <WEB>

A:Cross-references: GB:U04053; EMBL:M19350; NID:gl877426; PIDN:AAAC48868.1; PID:gl8774

R:Nelson, R.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.

J. Exp. Med. 174, 1271-1274, 1991

A:Title: Characterization and clonal distribution of four alleles of the speA gene en

A:Reference number: S18782; MUID:92044323; PMID:1940804

A:Accession: S18782

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 9-244 <NEA>

A:Cross-references: EMBL:X61560; NID:g47287; PIDN:CAA43758.1; PID:g47288

A:Experimental source: Streptococcus pyogenes strain MGAS156 isolate Nebraska unassign

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199

A:Accession: S18784

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 9-244 <NEA>

A:Cross-references: EMBL:X61556; NID:g47291; PIDN:CAA43754.1; PID:g47292

A:Experimental source: Streptococcus pyogenes strain MGAS165 isolate Minnesota unassign

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199

A:Accession: S18785

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 9-244 <NEZ>

A:Cross-references: EMBL:X61559; NID:g47293; PIDN:CAA43757.1; PID:g47294

A:Experimental source: Streptococcus pyogenes strain MGAS167 isolate Texas unassigned

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199

A:Accession: S18791

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 9-244 <NEY>

A:Cross-references: EMBL:X61555; NID:g47309; PIDN:CAA43753.1; PID:g47310

A:Experimental source: Streptococcus pyogenes strain MGAS327 isolate Arizona unassign

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199

A:Accession: S18796

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 9-244 <NEO>

A:Cross-references: EMBL:X61557; NID:g47319; PIDN:CAA43755.1; PID:g47320

A>Note: the nucleotide sequence was submitted to the EMBL Data Library.
A:Accession: S18794
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NE>
A:Cross-references: EMBL:X61570; NID:q47315; PIDN:CAAA43768.1; PID:q47316
A:Experimental source: strain MGAS491 isolate United Kingdom unassigned
A>Note: the nucleotide sequence was submitted to the EMBL Data Library.
A:Accession: S18801
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NE>
A:Cross-references: EMBL:X61572; NID:q47333; PIDN:CAAA3770.1; PID:q47334
A:Experimental source: strain MGAS524 isolate Germany unassigned phage
A>Note: the nucleotide sequence was submitted to the EMBL Data Library.
A:Accession: S18798
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NE>
A:Cross-references: EMBL:X61571; NID:q47323; PIDN:CAAA3769.1; PID:q47324
A:Experimental source: strain MGAS495 isolate Germany unassigned phage
A>Note: the nucleotide sequence was submitted to the EMBL Data Library.

```
C; Genetics:
A; Gene: speA3
C; Superfamily: enterotoxin B
C; Keywords: exotoxin
F; 1-22/Domain: signal sequence predicted <SIG>
F; 23-236/Product: exotoxin type A (fragment) #status predicted <MAT>

Query Match          93.6%;   Score 1238; DB 2; Length 236;
Best Local Similarity 99.2%;   Pred: No. 1.2e-85;
Matches 234; Conservative 1; Mismatches 1; Indels 0; Gaps 0

QY      9 KKMVFVLVFTFGLTISOEVAQQDPDPSQLHRSLSVKNLQNIVFLYEGDPVTHENVK
Db       1 KKMVFVLVFTFGLTISOEVAQQDPDPSQLHRSLSVKNLQNIVFLYEGDPVTHENVK
QY     69 DOLLSHLLIYNVSGPNYDKLTELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAEKRS
Db     61 DQLLSHDLLIYNVSGPNYDKLTELKNQEMATLFKDKNLDIYGVEYYHLCYLCENAEKRS
QY    129 IYGGVTNHGHNLETPKKIIVKVVSIDGTQSI.SFDIETNKKMVTQAELDYKVRKYLTDN
Db    121 IYGGVTNHGHNLETPKIIVKVVSIDGTIQSISFDIETNKKMVTQAELDYKVRKYLTDN
QY    189 LYTNGPSKYETGYIKFIPIKNKESFWFFDFPEPPTQSQILMIYADNTLDSNTSQI 2
```

161 LIINGFSKIEUIG.IIRIFANNESFWDFPFEPIQSNLEIIRKADLEIDONISQI

RESULT 3
S18786

extotoxin type A precursor (allele 2) - Streptococcus pyogenes phage (str N;Alternate names: scarlet fever toxin
C;Species: Streptococcus pyogenes
A;Variety: Streptococcus pyogenes California; strain MGAS251 isolate Cal
isolate United Kingdom; strain MGSA496 isolate Germany
C;date: 29-Jan-1993 #sequence revision 29-Jan-1993 #text change 16-Jul-1
C;Accession: S18786; S18787; S18788; S18790; S18792; S18795; S18799
R;Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A;Title: Characterization and clonal distribution of four alleles of the
A;Reference number: S18783; MUID:92044323; PMID:1940804
A;Accession: S18786
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NBL>
A;Cross-references: EMBL:X61561; NID:q47297; PID:CAA43759,1; PID:q47298
A;Experimental source: strain MGAS250 isolate California unassigned phag
A;Note: the nucleotide sequence was submitted to the EMBL Data Library,
A;Accession: S18787
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

C>Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999

C/Accession: S18789

R/Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.

J. Exp. Med. 174, 1271-1274, 1991

A/Title: Characterization and clonal distribution of four alleles of the *speA* gene

A/Reference number: S18782; MUID:92044323; PMID:1940804

A/Accession: S18789

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-236 <NEL>

A/Cross-references: EMBL:X61573; NID:947303; PIDN:CAA43771.1; PID:947304

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, September 19

C/Genetics:

C/Superfamily: enterotoxin B

C/Keywords: exotoxin

E/1-22/Domain: signal sequence (fragment) #status predicted <SIG>

F/23-236/Product: exotoxin A (fragment) #status predicted <NA>

Query Match 83.7%; Score 1108; DB 2; Length 236;

Best Local Similarity 88.6%; Pred. No. 6.7e-76;

Matches 209; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

Qy 9 KKWFFVLVFLGLTISQEVTAQDDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 68

Db 1 KKIYVFLAIPLGTTISQEVFAQDDPNPSQLHRSSLVKNLQNIYFLYEGDPVYHENVKSV 60

Qy 69 DQLSLHLIYVSGPNYDKLTKLNQEMATLFDKKNVDIYGVEYHLYCLENASAC 128

Db 61 DQLSLHLIYVSGUNYDKLTKLNREMSLTFKNKNVDIYGVEYHLYCLENARRAC 120

Qy 129 IYGVVTHNHNHLEIPKKIVVKVSDIGISQISFSDIETNKKMWTAGELDYKVKYLTDNKQ 188

Db 121 IYGVVTHNHNHLEIPKNILVKVSDIGISQISFSDIETSKMKMWTAGELDYKVKRHLTDNKQ 180

Qy 189 LYTNGPSKIETGYIKFIPKNKESWFDFPFEPFQSKYLMYIKDNEFLDSNTSQI 244

Db 181 LYTNGPSKIETGYIKFISKQETFWDFPFEPFNQVLYMIYIKDNETLDSSTSQI 236

RESULT 5

A26152

streptococcal pyrogenic exotoxin type A precursor - Streptococcus sp.

N/Alternate names: scarlet fever toxin; SPE type A (speA)

C/Species: Streptococcus sp.

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C/Accession: A26152

R/Johnson, L.P.; L'Italian, J.J.; Schlievert, P.M.

Mol. Gen. Genet. 203, 354-356, 1986

A/Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to

A/Reference number: A26152; MUID:86284313; PMID:3526093

A/Accession: A26152

A/Molecule type: DNA

A/Residues: 1-250 <JOH>

C/Superfamily: enterotoxin B

C/Keywords: exotoxin

Query Match 81.2%; Score 1074.5; DB 1; Length 250;

Best Local Similarity 83.7%; Pred. No. 2.3e-73;

Matches 210; Conservative 7; Mismatches 33; Indels 1; Gaps 1;

Qy 1 MNNKKVLKKWFFVLVFLGLTISQEVFAQDDPSQLHRSSLVKNLQNIYFLYEGDPV 60

Db 1 MNNKEVLKKWFFVLVFLGLTILPKGICSTRPKPSQLORSNLVKTFFIYFEMRVLV 60

Qy 61 THENVKSDQLLSHLHIYVSGPNYDKLTKLNQEMATLFDKKNVDIYGVEYHLYC 120

Db 61 THENVKSDQLLSHLHIYVSGPNYDKLTKLNQEMATLFDKKNVDIYGVEYHLYC 120

Qy 121 ENAERSACIYGVVTHNHNHLEIPKKIVVKVSDIGISQISFSDIETNKKMWTAGELDYKVR 180

Db 121 ENAERSACIYGVVTHNHNHLEIPKKIVVKVSDIGISQISFSDIETNKKMWTAGELDYKVR 179

us-09-308-830a-13.rpr

Db	131	SHQTDKRRKTCMYGCVTEHNGNQLDKYRSITVRFEDGKNLLSFQVQNKKKVTAQEL
QY	179	VRYKLTNKKLYTNGSPSKYETGYIKFIPKNESEWFFDFPEP--EFTQSKYLMAYKD
Db	191	TRHLVNVKKLYIFENNSPETYGTGIYKFI--ENESFYIWNMPAGDKFQDSKYLMMYND
QY	237	LDSNTSQIEVYLTATK 251
Db	250	VDSKDVRIEYLTATK 264

RESULT 7
S11885
enterotoxin C3 - *Staphylococcus aureus*
S11885
C:Species: *Staphylococcus aureus*
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1997
C:Accession: S11885
R:Howde, C.J.; Hackett, S.P.; Bohach, G.A.
Mol. Gen. Genet. 220, 329-333, 1990
A:Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene:
A:Reference number: S11885; MUID:90220508; PMID:2335627

Mol. Gen. Genet. 220: 329-333, 1990.

A:Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene:

A:Reference numbers: S11885; MUID:9020508; PMID:2325627

A:Accession: S11885

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-266 <HOV>

A:Cross references: GB:X51661; NID:g46570; PIDN:CAA35972.1; PID:g46571

C:Superfamily: enterotoxin B

[illegible]

126	QY	----	SACIYGVNTHBGNHLETP--KKIWKVKSIDGTSISFDIETNKKMVTQAQELD
			: : : : : : : : :
131	DB		VTGGKTCWGGIYKTBEGNFDNGNLQNVLYRVYENKRNITSEFQVDDKFSVTAQELD
			: : : : : : : :
180	QY		KKYLTNDKQLYTNGPSKYETGYIKFIPKNKESFDFDFPEP--EFTQSKYLMTYKDN
			: : : : : : : :
191	DB		RNFELINKNDIYFNSSPYETGYIKETIENNGTWFYDMMPAPGKDFQSKYLAMYN
			: : : : : : :
238	QY		DSNTSQIEVYLTTK 251
			: :
251	DB		DSKSVKTEVHLTTK 264
			: :

C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 16-Jul-1992
C;Accession: A60114; B60114; A33866
R;Bohach, G.A.; Schlievert, P.M.
Infect. Immun. 57, 2249-2252, 1989
A;Title: Conservation of the biologically active portions of staphylococcal surface-associated protein A.
A;Reference number: A60114; UID:89277549; PMID:2543637

A:Accession: A60114
 A:Title: Conservation of the biologically active portions of staphyloco-
 A:Reference number: A60114; MUID:89277549; PMID:2543637
 A:Residues: 1-266 <BOH>
 A:Molecule type: DNA
 A:Status: not compared with conceptual translation
 A:Residues: 1-266 <BOH>
 A:Accession: B60114
 A:Molecule type: protein
 A:Residues: 28-66 <BOH2>
 A:Residues: 28-66 <BOH2>
 A:Couch, J.L.; Betley, M.J.

R; Bayles, K.W.; Iandolo, J.J.
J. Bacteriol. 171, 4799-4806, 1989
A; Title: Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin
A; Reference number: A33953; MUID: 993359112; PMID: 2549000
A; Accession: A33953
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-258 <BAY>
A; Cross-references: GB:M28521; NID: g1492109; PID: AAB06195.1; PID: g758591
C; Superfamily: enterotoxin B

Query Match	26.1%;	Score 345;	DB 2;	Length 258;
Best Local Similarity	35.6%;	Pred. No. 1,le-18;		
Matches	93;	Conservative 47;	Mismatches 101;	Indels 20; Gaps 10;
Qy	8	LKKM-VFFVLVTFGLTTSQ-EVFAQQDPD---PSQLHR-----SSLVKNLQNIYFLVEG	57	
Db	1	MKFFNLTALLFFTSVLVSPLNVKANENIDSVKEKLHKKSELSTALNNKH5Y--ADK	58	
Qy	58	DPVTHENVKSDOLLSHHLLYN---VSGPNYDKLTKELKNOEMATLPKDNVDIYGYEY	114	
Db	59	NPIGENKSGDQPLENTLLKFKFTDLINFEDLLINFNSKEMAQHFKNVDVPYRYS	118	
Qy	115	HLCLCENAESACIYGGVNVNHEGNHLEIPKIKVKSIDIGIO-SLSFD-IETNKKMVA	172	
Db	119	INCYGGE-IDRTACTYGGVPHGEGNLUKEKKRPIPNLWINGQVEVSLDRVQTDKKNVT	177	
Qy	173	QELDYKVRKYJTDNKKLYTRGP--SKYETGYIFIPKNKESFWDFPEPEFFQSKVLM	230	
Db	178	QELDAQARRYLQDKLKYNDLTGGKIQRCCKIEFSDSGSKVSYDLDVFKGDPPEKQ	237	
Qy	231	YKDNETLDSNTSQIEVLYTTK	251	
Db	238	YSONKTLSTELHLDIYLYEK	258	

RESULT 12
C89984
enterotoxin P [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: C89984
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogawa, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; PMID:21311952; PMID:11418146
A:Accession: C89984
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-260 <KUR>
A:CROSS-references: GB:BA000018; PID:g13701743; PIDN:BAB43036.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: sep
C:Superfamily: enterotoxin B

Query Match	25.8%	Score 341;	DB 2;	Length 260;
Best Local Similarity	34.5%;	Pred. No. 2.3e-18;		
Matches	92;	Conservative 52;	Mismatches 85;	Indels 38; Gaps 13:
Qy	10	KWFFVLVTFGLTI-----	SOEYFAQQDDPSOLHRSSLVKNLQNIYFLYEGD	58
Db	1	: : : :	: : : :	: : : :
	5	KKTTFILLSFIALTLITSPFVNSKSEETNGDKLQKSELQGTAL-SNLRTQYV--HNGS		62
Qy	59	PVTHENVKSVQDLLSHHLLIYN--	VSGPN-YDKLKTCLKNCEMATLFKDKKNVDIYGVYYH	115
Db	63	AII-ENKESNDQFLKWTILFNDFFTGHQVNDLLVDLGSKDTANIYKGGKVDLYGVY--		119
Qy	116	LCYLCENAE--RSACTIYGVNTEHGNHLEIPKKIIVKVSIDIGTQSL--	SPDIETNKKWVT	171
Db	120	-GQCTGGTTPFKTACMGGVTLHDNNQLEEEKVPINLWDIGKQNTVPLGTVTKTNKEVT		178

```

Qy 172 AQELDYYKVRKYLTDNKQLYT----NGSKSYETGYIKFKPKNKESFWDFEPEPEPTQ
Db 179 VQELDQSRHYLHETYNLYNTDAFNG--KIQKGLIEFHPSSGDSVGYDLFG----AQ
Qy 228 ----LMIYKRDNETLDSNTSQIEVLYLT 250
Db 233 PDTQLRIYRDNKTIKSNMHIIDLYLT 259

RESULT 13
A89969
enterotoxin YENT2 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2-2001
C:Accession: A89969
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.;
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.
C:Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus
A:Reference number: A89758; PMID:21311952; PMID:11418146
A:Accession: A89969
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <KUR>
A:Cross-references: GB:BA000018; PID:g13701619; PIDN:BAB42912.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: yent2

```

Query Match		25.5%	Score 337;	DB 2;	Length 136;
Best Local Similarity		49.6%;	Pred. No. 2e-18;		
Matches	67;	Conservative	22;	Mismatches	38; Indels 8; Gaps
QY	125	RSACIYGVTWHEGNHL-----BIPKKIVVKVSI	DG IQSLSDIETNKKMTAQEID		
Db	2	KRTCMYGVTGEHDGNQDKNNSTDSNINILIKVYENRNSLSFDIPTNKKNTAQEID			
QY	179	VRYKVIITDNKOYLTCNGPSKIETGYGIKFTPKKNESFWE	DFPPE--PERTQSKYLMIKVDNR		
Db	62	VRNYLLKHKNLYENSNSPYETGYIKFTEGSGHSDFLMPESGCKFYPTKYLLIYNDR			
QY	237	LDSNTSQIEVYLTTK	251		
Db	122	VEKSINVEVHLT	TKK 136		

RESULT 14
E89969
enterotoxin SeO [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2010
C:Accession: E89969
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus
A:Reference number: A89758; MUID:213111952; PMID:11418146
A:Accession: E89969
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-260 <NR>
A:CROSS-references: GB:BA000018; PFD:gl3701623; PIDN:BAB42916.1; GSPDB:GN
A:Experimental source: strain N315
C:Genetics:
A:Gene: seo
C:Superfamily: enterotoxin B

Query Match 25.5%; Score 337; DB 2; Length 260;
Best Local Similarity 36.2%; Pred. NO. 4.5e-18;
Matches 96; Conservative 42; Mismatches 107; Indels 20; Gaps

RESULT 15

Query Match 23.9% Score 316.5 DB 2: Length 258:

Search completed: August 21, 2003, 12:50:19
Job time : 37 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 21, 2003, 12:14:04 ; Search time 74 Seconds
(without alignments)
875.287 Million cell updates/sec

Title: US-09-308-830A-13

Perfect score: 1323

Sequence: 1 MNNKKVLKRWFFVLVTL.....KDNELTDSNTSQIEVYLTK 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1313	99.2	251	16	Q8K6K5
2	1239	93.7	236	2	P97163
3	1238	93.6	236	2	Q54779
4	1233	93.2	236	2	Q57453
5	1172	88.6	222	2	Q9R931
6	1108	83.7	236	2	Q54696
7	1053	79.6	222	2	Q9S524
8	1053	79.6	222	2	Q938P4
9	554	41.9	271	2	Q9F0L6
10	552	41.7	266	16	Q8NXJ6
11	550	41.6	239	2	Q53678
12	549	41.5	239	2	Q06532
13	548	41.4	239	2	Q06533
14	547	41.3	239	2	Q05157
15	547	41.3	239	2	Q06531
16	543	41.0	239	2	Q06535

17	538	40.7	239	2	Q06534
18	537	40.6	234	2	Q9R5X4
19	535.5	40.5	260	2	Q54971
20	530.5	40.1	260	2	Q54738
21	530.5	40.1	260	16	Q54739
22	516.5	39.0	259	2	Q936G4
23	470	35.5	258	2	Q92NF2
24	470	35.5	258	2	Q9EZM3
25	468	35.4	233	2	Q8RR77
26	341	25.8	260	16	Q99SU3
27	338.5	25.6	261	2	Q9EZM8
28	337	25.5	136	16	Q99T49
29	337	25.5	260	16	Q99T46
30	316.5	23.9	258	16	Q9EZM4
31	315	23.8	250	2	Q8GFM6
32	312	23.6	260	16	Q931M4
33	304.5	23.0	240	16	Q9F0L7
34	304.5	23.0	268	2	O85217
35	303.5	22.9	240	16	O8NXJ5
36	298.5	22.6	241	16	Q53585
37	285.5	21.6	108	2	Q9EZM5
38	281.5	21.3	217	2	Q8RR76
39	270	20.4	239	16	Q99T47
40	269	20.3	239	2	Q9EZM7
41	259.5	19.6	242	16	Q8NVM2
42	257.5	19.5	242	2	O54476
43	255.5	19.3	242	2	Q93CC5
44	246.5	18.6	256	2	Q8VLW7
45	246	18.6	229	16	Q8NWX7

ALIGNMENTS

RESULT 1

Q8K6K5	ID	Q8K6K5	PRELIMINARY;	PRT;	251 AA.
AC	Q8K6K5;				
DT	01-OCT-2002 (TReMBLrel. 22, Created)				
DT	01-OCT-2002 (TReMBLrel. 22, Last sequence update)				
DT	01-MAR-2003 (TReMBLrel. 23, Last annotation update)				
DE	Exotoxin type A-phase associated.				
GN	SPEA3 OR SPYM3_1301.				
OS	Streptococcus pyogenes (serotype M3).				
OC	Bacteria: Firmicutes; Lactobacillales; Streptococcaceae;				
OC	Streptococcus				
OX	NCBI_taxid=198466;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-MGAS315 / Serotype M3;				
RX	MEDLINE=22133808; PubMed=12122206;				
RA	Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,				
RA	Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,				
RA	Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,				
RA	Schlievert P.M., Musser J.M.;				
RT	"Genome sequence of a serotype M3 strain of group A Streptococcus:				
RT	phage-encoded toxins, the high-virulence phenotype, and clone				
RT	emergence."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).				
DR	EMBL; AE014161; AA079908.1; -				
DR	InterPro; IPR006177; Bctrl_tox.				
DR	InterPro; IPR006123; Staph/Strep_toxin.				
DR	InterPro; IPR006126; Staph/Strep_tox.				
DR	InterPro; IPR006173; Staph_tox_OB.				
DR	Pfam; PF01123; Staph_Strep_toxin; 1.				
DR	Pfam; PF02876; Staph_Strep_tox_C; 1.				
DR	PRINTS; PR00279; BACTRLTOXIN.				
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.				
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.				
KW	Complete proteome.				
SQ	SEQUENCE 251 AA; 29260 MW; 05E782CDA01BFCD5 CRC64;				
Query Match	99.2%;	Score	1313;	DB	16; Length 251;

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Best Local Similarity 99.2%; Pred. No. 1.3e-85;
Matches 249; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNNKVKLVKMYFFVLTGLTISQEVFAQQDDPSQLHRSSLVKLNQNIYFLYEGDPV 60
Db 1 MNNKVKLVKMYFFVLTGLTISQEVFAQQDDPSQLHRSSLVKLNQNIYFLYEGDPV 60
QY 61 THENKVSVDQLSHHLYNVSGPNYDKLTKELKNOEMATLFDKNDVYIGVEYHLCYIC 120
Db 61 THENKVSVDQLSHHLYNVSGPNYDKLTKELKNOEMATLFDKNDVYIGVEYHLCYIC 120
QY 121 ENAERSACIYGVTHNHNHLEIPKKIVVKSIDIGISLSDIETNKKMVTAEQELDYKVR 180
Db 121 ENAERSACIYGVTHNHNHLEIPKKIVVKSIDIGISLSDIETNKKMVTAEQELDYKVR 180
QY 181 KVLTKNOLYTNKPSKYETGYIKFIPKNKESFWDFEPEFTQSKYLMYKDNETLDSN 240
Db 181 KVLTKNOLYTNKPSKYETGYIKFIPKNKESFWDFEPEFTQSKYLMYKDNETLDSN 240
QY 241 TSQIEVYLTTK 251
Db 241 TSQIEVYLTTK 251

RESULT 2
P97163
ID P97163 PRELIMINARY; PRT: 236 AA.
AC Q54779; Q54736; Q54740; Q54741;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAY-2003 (TREMBLrel. 23, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN SPCA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS156, and MGAS500;
RX MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Selaender R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
Streptococcus pyogenes."
RT J. Exp. Med. 174:1271-1274(1991).
RL EMBL; X61556; CAA43754.1; -
DR EMBL; X61557; CAA43755.1; -
DR EMBL; X61560; CAA43758.1; -
DR EMBL; X61555; CAA43753.1; -
DR EMBL; X61558; CAA43756.1; -
DR EMBL; X61559; CAA43757.1; -
DR EMBL; X61554; CAA43752.1; -
DR HSP; P08095; 1B1Z.
DR InterPro; IPR006177; Bcrl.tox.
DR InterPro; IPR006123; Stap/Strep.toxin.
DR InterPro; IPR006126; Staph/Strep.tox.
DR InterPro; IPR006173; Staph.tox.OB.
DR Pfam; PF01123; Stap.Strp.toxin; 1.
DR Pfam; PF02876; Stap.Strp.tox.C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27454 MW; 3FB3F41ABDC13A84 CRC64;

Query Match 99.7%; Score 1239; DB 2; Length 236;
Best Local Similarity 99.6%; Pred. No. 2.1e-80;
Matches 235; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNNKVKLVKMYFFVLTGLTISQEVFAQQDDPSQLHRSSLVKLNQNIYFLYEGDPV 68
Db 1 MNNKVKLVKMYFFVLTGLTISQEVFAQQDDPSQLHRSSLVKLNQNIYFLYEGDPV 68
QY 61 THENKVSVDQLSHHLYNVSGPNYDKLTKELKNOEMATLFDKNDVYIGVEYHLCYIC 128
Db 61 THENKVSVDQLSHHLYNVSGPNYDKLTKELKNOEMATLFDKNDVYIGVEYHLCYIC 128
QY 121 ENAERSACIYGVTHNHNHLEIPKKIVVKSIDIGISLSDIETNKKMVTAEQELDYKVR 180
Db 121 ENAERSACIYGVTHNHNHLEIPKKIVVKSIDIGISLSDIETNKKMVTAEQELDYKVR 180
QY 181 KVLTKNOLYTNKPSKYETGYIKFIPKNKESFWDFEPEFTQSKYLMYKDNETLDSN 244
Db 181 KVLTKNOLYTNKPSKYETGYIKFIPKNKESFWDFEPEFTQSKYLMYKDNETLDSN 244
QY 241 TSQIEVYLTTK 251
Db 241 TSQIEVYLTTK 251

RESULT 3
Q54779
ID Q54779 PRELIMINARY; PRT: 236 AA.
AC Q54779; Q54736; Q54740; Q54741;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAY-2003 (TREMBLrel. 23, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN SPCA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS624 AND MGAS158 AND MGAS485 AND MGAS491, and MGAS495;
RX MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Selaender R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
Streptococcus pyogenes."
RT J. Exp. Med. 174:1271-1274(1991).
RL EMBL; X61569; CAA43767.1; -
DR EMBL; X61572; CAA43770.1; -
DR EMBL; X61568; CAA43766.1; -
DR EMBL; X61570; CAA43768.1; -
DR EMBL; X61571; CAA43769.1; -
DR HSP; P08095; 1B1Z.
DR InterPro; IPR006177; Bcrl.tox.
DR InterPro; IPR006123; Stap/Strep.toxin.
DR InterPro; IPR006126; Staph/Strep.tox.
DR InterPro; IPR006173; Staph.tox.OB.
DR Pfam; PF01123; Stap.Strp.toxin; 1.
DR Pfam; PF02876; Stap.Strp.tox.C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27468 MW; 29DF2AD575623A84 CRC64;

Query Match 93.6%; Score 1238; DB 2; Length 236;
Best Local Similarity 99.2%; Pred. No. 2.5e-80;
Matches 234; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 KMWFFVLVTLGLTISQEVFAQQDDPSQLHRSSLVKLNQNIYFLYEGDPVTHENVKSV 68
Db 1 KMWFFVLVTLGLTISQEVFAQQDDPSQLHRSSLVKLNQNIYFLYEGDPVTHENVKSV 68
QY 69 DQLSHHLYNVSGPNYDKLTKELKNOEMATLFDKNDVYIGVEYHLCYICENASAC 128
Db 69 DQLSHHLYNVSGPNYDKLTKELKNOEMATLFDKNDVYIGVEYHLCYICENASAC 128
QY 121 ENAERSACIYGVTHNHNHLEIPKKIVVKSIDIGISLSDIETNKKMVTAEQELDYKVR 180
Db 121 ENAERSACIYGVTHNHNHLEIPKKIVVKSIDIGISLSDIETNKKMVTAEQELDYKVR 180
QY 181 KVLTKNOLYTNKPSKYETGYIKFIPKNKESFWDFEPEFTQSKYLMYKDNETLDSN 236
Db 181 KVLTKNOLYTNKPSKYETGYIKFIPKNKESFWDFEPEFTQSKYLMYKDNETLDSN 236

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Qy 129 IYGVNTNHEGHLIEPKKIVVKSIDIGISLSEFDTETNKKMTAQLDYKVRKYLTDNQ 188
Db 121 IYGVNTNHEGHLIEPKKIVVKSIDIGISLSEFDTETNKKMTAQLDYKVRKYLTDNQ 180

Qy 189 LYTGNSKYETGYIKFIPKNKESFWDFPEFTQSKYLMYKDNETLDSNTSQI 244
Db 181 LYTGNSKYETGYIKFIPKNKESFWDFPEFTQSKYLMYKDNETLDSNTSQI 236

RESULT 4
Q57453
ID Q57453 PRELIMINARY; PRT; 236 AA.
AC Q57453;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS496;
RX MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes.";
RL J. Exp. Med. 174:1271-1274 (1991).
DR EMBL; X61562; CAA43760.1; -
DR EMBL; X61563; CAA43761.1; -
DR EMBL; X61567; CAA43765.1; -
DR EMBL; X61561; CAA43759.1; -
DR EMBL; X61564; CAA43762.1; -
DR EMBL; X61565; CAA43763.1; -
DR EMBL; X61566; CAA43764.1; -
DR HSP; P08095; IBI2.
DR InterPro; IPR006177; BcTrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1 1
FT CHAIN <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27484 MW; 2EF7P41AAC853600 CRC64;

Query Match 93.2%; Score 1233; DB 2; Length 236;
Best Local Similarity 99.2%; Pred. No. 5.6e-80;
Matches 234; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 KKMVFVLTFLGLTISQEVFAQQDDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 68
Db 1 KKMVFVLTFLGLTISQEVFAQQDDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 60

Qy 69 DQLLSHLIYNVSGPNVDKLTCLKNOEMATLFKDKNVDIYGYEYHLCVLCENASRSAC 128
Db 61 DQLLSHLIYNVSGPNVDKLTCLKNOEMATLFKDKNVDIYGYEYHLCVLCENASRSAC 120

Qy 129 IYGVNTNHEGHLIEPKKIVVKSIDIGISLSEFDTETNKKMTAQLDYKVRKYLTDNQ 188
Db 121 IYGVNTNHEGHLIEPKKIVVKSIDIGISLSEFDTETNKKMTAQLDYKVRKYLTDNQ 180

Qy 189 LYTGNSKYETGYIKFIPKNKESFWDFPEFTQSKYLMYKDNETLDSNTSQI 244

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Db 181 LYTGNSKYETGYIKFIPKNKESFWDFPEFTQSKYLMYKDNETLDSNTSQI 236

RESULT 5
Q9R931
ID Q9R931 PRELIMINARY; PRT; 222 AA.
AC Q9R931;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Exotoxin A (Fragment).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D709;
RX MEDLINE=99137798; PubMed=9952369;
RA Bessen D.E., Izzo M.W., Fiorentino T.R., Carling R.M.,
RA Hollingshead S.K., Beall B.;
RT "Genetic linkage of exotoxin alleles and emm gene markers for tissue
RT tropism in group A streptococci.";
RL J. Infect. Dis. 179:627-636 (1999).
DR EMBL; AF055698; AAD11624.1; -
DR HSP; P08095; IBI2.
DR InterPro; IPR006177; BcTrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1 1
FT NON_TER 222 222
SQ SEQUENCE 222 AA; 25759 MW; 48BB7ADDCD91FBA3 CRC64;

Query Match 88.6%; Score 1172; DB 2; Length 222;
Best Local Similarity 99.5%; Pred. No. 1.1e-75;
Matches 221; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 21 GLTISQEVFAQQDDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLSSHLYNV 80
Db 1 GLTISQEVFAQQDDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLSSHLYNV 60

Qy 81 SGPNDKLTCLKNOEMATLFKDKNVDIYGYEYHLCVLCENASRSACIYGGVTHHEGNH 140
Db 61 SGPNDKLTCLKNOEMATLFKDKNVDIYGYEYHLCVLCENASRSACIYGGVTHHEGNH 120

Qy 141 LEIPKKIVVKSIDIGISLSEFDTETNKKMTAQLDYKVRKYLTDNQKQYNGPSKYETG 200
Db 121 LEIPKKIVVKSIDIGISLSEFDTETNKKMTAQLDYKVRKYLTDNQKQYNGPSKYETG 180

Qy 201 YIKFIPKNKESFWDFPEFTQSKYLMYKDNETLDSNTS 242
Db 181 YIKFIPKNKESFWDFPEFTQSKYLMYKDNETLDSNTS 222

RESULT 6
Q54696
ID Q54696 PRELIMINARY; PRT; 236 AA.
AC Q54696;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

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OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS156;
RX MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Selaender R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes.";
RL J. Exp. Med. 174:1271-1274(1991).
DR EMBL; X61573; CAA43771.1; -
DR HSP; P08095; 1B12.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Stap/Strep_toxin.
DR InterPro; IPR006126; Staph/Strept_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Stap_Strp_toxin; 1.
DR Pfam; PF02876; Stap_Strp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 222
SQ SEQUENCE 236 AA; 27575 MW; 70F54120E79127DF CRC64;

Query Match 83.7%; Score 1108; DB 2; Length 236;
Best Local Similarity 88.6%; Pred. No. 4.1e-71;
Matches 209; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 9 KKMVEFVLTFLGLTISQEVFAQQDPNPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 68
DB 1 KKIVYFLAIFLGLTTSQEVFAQQDPNPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 60

QY 69 DQLSHHLIYNVSGPNYDKLTKELKNOEMATLFDKKNVDIYGVYHYHLYCLCENASRAC 128
DB 61 DQLSHDLIYNVSGLYNDKLTCLKNREMSLTFKKNVDIYGVYHYHLYCLCRNAKRAC 120

QY 129 IYGVNTHNHEGNHLEIPKKIVKVSIDGIQSLSPDIETNKKMVTQAQELDYKVRKYLTDNKKQ 188
DB 121 IYGVNTHNHEGNHLEIPKNILVKVSIDGIQSLSPDIETSKKMVTQAQELDYKVRKHLTDNKKQ 180

189 LYTNGPSKYETGYIKPIPKNKSEFWDFPEPEFTQSKYLMYKDNETLDSNTSQI 244
181 LYTNGPSKYETGYIKFISKDETFWDFPEPEFNQVKYLMYKDNETLDSNTSQI 236

RESULT 7
Q9S5Z4 PRELIMINARY; PRT; 222 AA.
AC Q9S5Z4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Exotoxin type A (Fragment).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D633;
RX MEDLINE=99137798; PubMed=9952369;
RA Bessen D.E., Izzo M.W., Fiorentino T.R., Caringal R.M.,
RA Hollingshead S.K., Beall B.;
RT "Genetic linkage of exotoxin alleles and emm gene markers for tissue
RT tropism in group A streptococci.";
RL J. Infect. Dis. 179:627-636(1999).
DR EMBL; AF029051; AAD21315.1; -
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DR HSP; P08095; 1B12.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Stap/Strep_toxin.
DR InterPro; IPR006126; Staph/Strept_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Stap_Strp_toxin; 1.
DR Pfam; PF02876; Stap_Strp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 222
SQ SEQUENCE 222 AA; 25884 MW; 121F8460992818F8 CRC64;

Query Match 79.6%; Score 1053; DB 2; Length 222;
Best Local Similarity 89.2%; Pred. No. 3e-67;
Matches 198; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 21 GLTISQEVFAQQDPNPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHHLIYN 1
DB 1 GLTTSQEVFAQQDPNPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHDLIYN 1

QY 81 SGPNTDKLTKELKNOEMATLFDKKNVDIYGVYHYHLYCLCENASRACIYGVNTHNHEGNH 1
DB 61 SGLNYDKLTKELKKNREMSLTFKKNVDIYGVYHYHLYCLCRNAKRACIYGVNTHNHEGNH 1

QY 141 LEIPKKIVKVSIDGIQSLSPDIETNKKMVTQAQELDYKVRKYLTDNKKQLYTNGPSKYETG 1
DB 121 LEIPKNILVKVSIDGIQSLSPDIETSKKMVTQAQELDYKVRKHLTDNKKQLYTNGPSKYETG 1

QY 201 YIKFIPKNKSEFWDFPEPEFTQSKYLMYKDNETLDSNTS 242
DB 181 YIKFISKDETFWDFPEPEFNQVKYLMYKDNETLDSNTS 222

RESULT 8
Q938P4 PRELIMINARY; PRT; 222 AA.
AC Q938P4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Pyrogenic exotoxin A (Fragment).
GN SPEA.
OS Streptococcus equisimilis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=119602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4951;
RA Kalia A., Bessen D.E.;
RT Isolates of group G streptococci.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY049745; AAL06068.1; -
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Stap/Strep_toxin.
DR InterPro; IPR006126; Staph/Strept_tox.
DR Pfam; PF01123; Stap_Strp_toxin; 1.
DR Pfam; PF02876; Stap_Strp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 222
SQ SEQUENCE 222 AA; 25884 MW; 121F8460992818F8 CRC64;

Query Match 79.6%; Score 1053; DB 2; Length 222;
Best Local Similarity 89.2%; Pred. No. 3e-67;
Matches 198; Conservative 12; Mismatches 12; Indels 0; Gaps 0;
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Qy 21 GLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDQLLSHLIYV 80
Db 1 GLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDQLLSHLIYV 60
Qy 81 SGPNDKLTTELKQEMATLFDKNDVIYGVYHYHLCYLCENASACIYGGVTHHGNH 140
Db 61 SGLNDKLTTELKQEMATLFDKNDVIYGVYHYHLCYLCENASACIYGGVTHHGNH 120
Qy 141 LEIPKIVKVSIDIGISLSDIETNKKWTAQELDYKVKRYLDNQLYNGSPSKYETG 200
Db 121 LEIPKIVKVSIDIGISLSDIETNKKWTAQELDYKVKRYLDNQLYNGSPSKYETG 180
Qy 201 YIKFIPKNKESFDFPEPEFTOSKYLMIYKDNELDSNTS 242
Db 181 YIKFIPKNKESFDFPEPEFTOSKYLMIYKDNELDSNTS 222
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RESULT 9

```
Q9F0L6 PRELIMINARY; PRT; 271 AA.
ID Q9F0L6;
AC Q9F0L6;
DT 01-MAR-2001 (TremBrel. 16, Created)
DT 01-MAR-2001 (TremBrel. 16, Last sequence update)
DT 01-MAR-2003 (TremBrel. 23, Last annotation update)
DE Staphylococcus aureus enterotoxin C-bovine.
GN SEC-BOV.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2056668; PubMed=11114901;
RA Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
RA Meaney W.J., Smyth C.J.;
RT "Characterization of a putative pathogenicity island from bovine
RT Staphylococcus aureus encoding multiple superantigens.";
RL J. Bacteriol. 183:63-70(2001).
DR EMBL; AF217235; AAG29599.1; -.
DR HSSP; P34071; 1SE2.
DR InterPro; IPR006177; Bcrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_toxin; 1.
DR Pfam; PF02876; Staph_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 271 AA; 31267 MW; 3493F6228B042F10 CRC64;
```

```
Query Match 41.9%; Score 554; DB 2; Length 271;
Best Local Similarity 44.9%; Pred. No. 9.3e-32;
Matches 115; Conservative 51; Mismatches 72; Indels 18; Gaps 8;

Qy 11 MVF-FVLVTFGLTISQEVFAQQDPDPSQLHRSSLVKNL-QNIYFLYEGDPVTHENVKSV 68
Db 17 LIFALILVLPFPNVLAEE---SOPDPTDELHKASKFTGLMENMKVLYDDRVSVATKVKSV 73
Qy 69 DQLLSHLIYVNSG---PNYDKLTELKQEMATLFDKNDVIYGVYHYHLCYLC--ENA 123
Db 74 DKFLAHLIYVNSDKLKNYDKVKTTELLNEDLAKYKDEVDVYVYNSYVNCYFSSKDNV 133
Qy 124 ER----SACIYGGVTNHEGHNLEIPK--KIVVKVYSIDIGISLSDIETNKKWTAQELDY 177
Db 134 GKVTGGKTCMYGGITKHEGHNFDNGKLNQNLVIRVYENKRNITISFEVQDKKSVTAQELDI 193
Qy 178 KVRKYLDNQLYNGSPSKYETGYIKFIPKNKESFDFPEPE--EFTQSKYLYMIYKDNK 235
Db 194 KARNFLNKKNLKLYEFNSSPYETGYIKFTIENNGNTFWYDMMPAPGDKFQSKYLYMMYNDNK 253
Qy 236 TLDNNTSQIEVYLTK 251
Db 254 TVDSKSKVIEVHLTK 269
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RESULT 10

```
Q8NXJ6 PRELIMINARY; PRT; 266 AA.
ID Q8NXJ6;
AC Q8NXJ6;
DT 01-OCT-2002 (TremBrel. 22, Created)
DT 01-OCT-2002 (TremBrel. 22, Last sequence update)
DT 01-MAR-2003 (TremBrel. 23, Last annotation update)
DE ENTEROTOXIN TYPE C PRECURSOR.
GN SEC4 OR MW0759.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMBL; AP004824; BAB94624.1; -.
DR InterPro; IPR006177; Bcrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_toxin; 1.
DR Pfam; PF02876; Staph_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 266 AA; 30670 MW; 4C654659AA48120F CRC64;
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Query Match 41.7%; Score 552; DB 16; Length 266;
Best Local Similarity 44.5%; Pred. No. 1.3e-31;
Matches 114; Conservative 51; Mismatches 73; Indels 18; Gaps 8;

Qy 11 MVF-FVLVTFGLTISQEVFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSV 68
Db 12 LIFALILVLPFPNVLAEE---SOPDPTDELHKSEFTGTGMNMYLYDDRVSVATKVKSV 68
Qy 69 DQLLSHLIYVNSG---PNYDKLTELKQEMATLFDKNDVIYGVYHYHLCYLC--ENA 123
Db 69 DKFLAHLIYVNSDKLKNYDKVKTTELLNEDLAKYKDEVDVYVYNSYVNCYFSSKDNV 128
Qy 124 ER----SACIYGGVTNHEGHNLEIPK--KIVVKVYSIDIGISLSDIETNKKWTAQELDY 177
Db 129 GKVTGGKTCMYGGITKHEGHNFDNGKLNQNLVIRVYENKRNITISFEVQDKKSVTAQELDI 188
Qy 178 KVRKYLDNQLYNGSPSKYETGYIKFIPKNKESFDFPEPE--EFTQSKYLYMIYKDNK 235
Db 189 KARNFLNKKNLKLYEFNSSPYETGYIKFTIENNGNTFWYDMMPAPGDKFQSKYLYMMYNDNK 248
Qy 236 TLDNNTSQIEVYLTK 251
Db 249 TVDSKSKVIEVHLTK 264
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RESULT 11

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Q53678 PRELIMINARY; PRT; 239 AA.
ID Q53678;
AC Q53678;
DT 01-NOV-1996 (TremBrel. 01, Created)
DT 01-NOV-1996 (TremBrel. 01, Last sequence update)
DT 01-MAR-2003 (TremBrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
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RP SEQUENCE FROM N.A.
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RL biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; L13376; AAA26620.1; -.
DR HSSP; P34071; ISE2.
DR InterPro; IPR006177; Bcstrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_toxin_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR NON_TER 1
SQ SEQUENCE 239 AA; 27618 MW; A13E7EB25C6989C2 CRC64;

Query Match 41.6%; Score 550; DB 2; Length 239;
Best Local Similarity 47.0%; Pred. No. 1.5e-31;
Matches 111; Conservative 45; Mismatches 66; Indels 14; Gaps 6;

QY 30 AQDDPDPQLHRSSLYKNL-QNIYFLYEGDPVTHENKVSVDQLSHHLYNVSG---PNY 85
DB 2 SQDPTPDELHKASKFTGLMNNKVLDDRYVSATKVSVDKFLAHLDIYNISDKKLNY 61
QY 86 DKLAKTELKNOEMATLFDKKNVDIYGVVEYHLCYLC--ENAEER---SACIYGGVTNHG 139
DB 62 DKVKTLLNEDLAKKYDEVVDVYGSNYVYCNFYSSKDNVGVTKGTCTMGGITKHGEG 121
QY 140 HLEIPK--KIVVVKVSDIGQISLFDIETNKKMVTQAQELDYKVRKYLTDNKLQYTNGPSK 197
DB 122 HFDNGNLQNLVLRVYENKRNITISFEVQTDKKSVTQAQELDIKARNFLINKNLYEFNSSP 181
QY 198 ETGYIKFIPKNKESFWDFFPEP--EFTQSKYLMYKDNETLDSNTSOIEVYLTTK 251
DB 182 ETGYIKFTENNGNTFWYDMMPAGDKFQSKYLMYNDNKTVDTSKSVKIEVHLTK 237

RESULT 12
Q06532 PRELIMINARY; PRT; 239 AA.
AC Q06532;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=740N;
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RL biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; L13375; AAA26619.1; -.
DR HSSP; P34071; ISE2.
DR InterPro; IPR006177; Bcstrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_toxin_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR NON_TER 1
SQ SEQUENCE 239 AA; 27642 MW; C77009F46BC8D645 CRC64;

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Query Match 41.5%; Score 549; DB 2; Length 239;
Best Local Similarity 47.0%; Pred. No. 1.8e-31;
Matches 111; Conservative 44; Mismatches 67; Indels 14; Gaps

QY 30 AQDDPDPQLHRSS-LVKNLQNIYFLYEGDPVTHENKVSVDQLSHHLYNVSG---PNY
DB 2 SQDPPMPDDLHKSSSEFTGTMNKMVLYDDHYVSATKVSVDKFLAHLDIYNISDKKLKN
QY 86 DKLAKTELKNOEMATLFDKKNVDIYGVVEYHLCYLC--ENAEER---SACIYGGVTNHG
DB 62 DKVKTLLNEDLAKKYDEVVDVYGSNYVYCNFYSSKDNVGVTKGTCTMGGITKHGEG
QY 140 HLEIP--KKIVVVKVSDIGQISLFDIETNKKMVTQAQELDYKVRKYLTDNKLQYTNGPSK
DB 122 HFDNGNLQNLVLRVYENKRNITISFEVQTDKKSVTQAQELDIKARNFLINKNLYEFNSSP
QY 198 ETGYIKFIPKNKESFWDFFPEP--EFTQSKYLMYKDNETLDSNTSOIEVYLTTK 251
DB 182 ETGYIKFTENNGNTFWYDMMPAGDKFQSKYLMYNDNKTVDTSKSVKIEVHLTK 237

RESULT 13
Q06533 PRELIMINARY; PRT; 239 AA.
AC Q06533;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MNCOpeland;
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RL biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; L13378; AAA26622.1; -.
DR HSSP; P34071; ISTE.
DR InterPro; IPR006177; Bcstrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_toxin_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR NON_TER 1
SQ SEQUENCE 239 AA; 27651 MW; A21A954386A8E625 CRC64;

Query Match 41.4%; Score 548; DB 2; Length 239;
Best Local Similarity 46.6%; Pred. No. 2.1e-31;
Matches 110; Conservative 45; Mismatches 67; Indels 14; Gaps

QY 30 AQDDPDPQLHRSS-LVKNLQNIYFLYEGDPVTHENKVSVDQLSHHLYNVSG---PNY
DB 2 SQDPTPDELHKSSSEFTGTMNKMVLYDDHYVSATKVSVDKFLAHLDIYNISDKKLKN
QY 86 DKLAKTELKNOEMATLFDKKNVDIYGVVEYHLCYLC--ENAEER---SACIYGGVTNHG
DB 62 DKVKTLLNEDLAKKYDEVVDVYGSNYVYCNFYSSKDNVGVTKGTCTMGGITKHGEG
QY 140 HLEIP--KKIVVVKVSDIGQISLFDIETNKKMVTQAQELDYKVRKYLTDNKLQYTNGPSK
DB 122 HFDNGNLQNLVLRVYENKRNITISFEVQTDKKSVTQAQELDIKARNFLINKNLYEFNSSP
QY 198 ETGYIKFIPKNKESFWDFFPEP--EFTQSKYLMYKDNETLDSNTSOIEVYLTTK 251
DB 182 ETGYIKFTENNGNTFWYDMMPAGDKFQSKYLMYNDNKTVDTSKSVKIEVHLTK 237

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Db 182 ETGYIKFIENNGNTFWYDMPAPGDKFDQSKYLMYNDNKTVDKRVKIEVHLTK 237
RESULT 14
O05157 PRELIMINARY; PRT; 239 AA.
AC O05157;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Type C enterotoxin (Fragment).
OS Staphylococcus intermedius.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1285;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-95-011195;
RA Edwards V.M., Deringer J.R., Callantine S.D., Deobald C.F.,
RA Berger P.H., Kapur V., Stauffer C.V., Bohach G.A.;
RT "Characterization of the type C enterotoxin (SEC-canine) produced by
RT Staphylococcus intermedius pyoderma isolates."
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RR EMBL; U91526; AAB50248.1;
RR HSP; P23313; LJCK
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
SQ SEQUENCE 239 AA; 27536 MW; D660644660DE4191 CRC64;

Query Match 41.3%; Score 547; DB 2; Length 239;
Best Local Similarity 47.5%; Pred. No. 2.5e-31;
Matches 112; Conservative 42; Mismatches 68; Indels 14; Gaps 6;

QY 30 AQQDPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVYDQLLSHLLIYNVSG---PNY 85
DB 2 SQDPPMPDDLKSEFTGTGNMKLYDDHYVSVATKVKSVKDFLAHLIYNISDKLKNY 61

QY 86 DLKLTENKQEMATFLKDKNDVIYGYEYHLCYLC--ENAE-----SACIYGGVTHNHN 139
DB 62 DKVTELLNEDLAKKYDEVVDYVGSNYVNCYFSSKDNVGVKGTCTMYGTTKHEGN 121

QY 140 HLEIP--KKIVKVSIDGQSLSFDIETNKKMTAQELDYKVKYLTDNKQLYTNGPSKY 197
DB 122 HFDGNLQNLVIRVYENKRNITISFVQTKKSVTAQELDIKARNFLINKNLYEFNSSPY 181

QY 198 ETGYIKFIENNGNTFWYDMPAPGDKFDQSKYLMYNDNKTVDKRVKIEVHLTK 251
DB 182 ETGYIKFIENNGNTFWYDMPAPGDKFDQSKYLMYNDNKTVDKRVKIEVHLTK 237

Search completed: August 21, 2003, 12:49:34
Job time : 76 secs
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Db 182 ETGYIKFIENNGNTFWYDMPAPGDKFDQSKYLMYNDNKTVDKRVKIEVHLTK 237
RESULT 14
O05157 PRELIMINARY; PRT; 239 AA.
AC O05157;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Type C enterotoxin (Fragment).
OS Staphylococcus intermedius.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1285;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-95-011195;
RA Edwards V.M., Deringer J.R., Callantine S.D., Deobald C.F.,
RA Berger P.H., Kapur V., Stauffer C.V., Bohach G.A.;
RT "Characterization of the type C enterotoxin (SEC-canine) produced by
RT Staphylococcus intermedius pyoderma isolates."
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RR EMBL; U91526; AAB50248.1;
RR HSP; P23313; LJCK
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
SQ SEQUENCE 239 AA; 27536 MW; D660644660DE4191 CRC64;

Query Match 41.3%; Score 547; DB 2; Length 239;
Best Local Similarity 47.5%; Pred. No. 2.5e-31;
Matches 112; Conservative 42; Mismatches 68; Indels 14; Gaps 6;

QY 30 AQQDPDPSQLHRSS-LVKNLQNIYFLYEGDPVTHENVKSVYDQLLSHLLIYNVSG---PNY 85
DB 2 SQDPPMPDDLKSEFTGTGNMKLYDDHYVSVATKVKSVKDFLAHLIYNISDKLKNY 61

QY 86 DLKLTENKQEMATFLKDKNDVIYGYEYHLCYLC--ENAE-----SACIYGGVTHNHN 139
DB 62 DKVTELLNEDLAKKYDEVVDYVGSNYVNCYFSSKDNVGVKGTCTMYGTTKHEGN 121

QY 140 HLEIP--KKIVKVSIDGQSLSFDIETNKKMTAQELDYKVKYLTDNKQLYTNGPSKY 197
DB 122 HFDGNLQNLVIRVYENKRNITISFVQTKKSVTAQELDIKARNFLINKNLYEFNSSPY 181

QY 198 ETGYIKFIENNGNTFWYDMPAPGDKFDQSKYLMYNDNKTVDKRVKIEVHLTK 251
DB 182 ETGYIKFIENNGNTFWYDMPAPGDKFDQSKYLMYNDNKTVDKRVKIEVHLTK 237

RESULT 15
O06531 PRELIMINARY; PRT; 239 AA.
AC O06531;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-4446;
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 21, 2003, 10:23:04 ; Search time 30 seconds
(without alignments)
393.457 Million cell updates/sec

Title: US-09-308-830A-13
Perfect score: 1323
Sequence: 1 MENNKVLLKMFVFLVTFLL.....KDNFTLDSNTSQIEVYLTK 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1314	99.3	251	1	SPEA_STRPY
2	575.5	43.5	266	1	ETXB_STAAU
3	550.5	41.6	266	1	ETC3_STAAU
4	548	41.4	266	1	ETC2_STAAU
5	547	41.3	266	1	ETC1_STAAU
6	480	36.3	258	1	ETXG_STAAU
7	345	26.1	258	1	ETXD_STAAU
8	313	23.7	257	1	ETXE_STAAU
9	312	23.6	257	1	ETXA_STAAU
10	214	16.2	235	1	SPEC_STRPY
11	213.5	16.1	236	1	SPFH_STRPY
12	162	12.2	234	1	SPFG_STRPY
13	116	8.8	234	1	TSST_STAAU
14	102.5	7.7	1790	1	USO1_YEAST
15	101	7.6	894	1	DSCL_HUMAN
16	100.5	7.6	396	1	PRRC_ECOLI
17	96	7.3	427	1	V55A_HSV7J
18	96	7.3	908	1	DPOL_BORBU
19	95.5	7.2	434	1	PURA_WIGBR
20	95.5	7.2	999	1	HGP2_HAEIN
21	95	7.2	554	1	Y478_RICPR
22	94.5	7.1	2151	1	RRPL_SEOUR
23	93	7.0	500	1	TACY_CLOPE
24	92.5	7.0	968	1	RNE_BUCAP
25	92	7.0	660	1	PRIA_BORBU
26	91.5	6.9	405	1	DBR1_YEAST
27	91	6.9	384	1	SCS7_YEAST
28	91	6.9	1956	1	ATX1_PLAFA
29	91	6.9	3255	1	POIG_LMVO
30	90.5	6.8	807	1	HISA_STAAU
31	90.5	6.8	3255	1	POIG_LMVE
32	90	6.8	286	1	Y907_METJA
33	90	6.8	376	1	CARA_WIGBR

34	90	6.8	440	1	STRP_STRPY	P10520 streptococc
35	89.5	6.8	439	1	NADB_CLOPE	Q8xne2 clostridium
36	89.5	6.8	642	1	SYT_BUCAP	P46244 buchnera ap
37	89	6.7	307	1	OPPE_STRP8	Q8p215 streptococc
38	88.5	6.7	487	1	DNLI_BPT6	P19088 bacterioph
39	88.5	6.7	495	1	Y243_AQUAE	O66606 aquifex aeo
40	88.5	6.7	540	1	MTAL_ACICA	P25201 acinetobact
41	88.5	6.7	993	1	HGBC_HAEIN	Q9k1v0 haemophilus
42	88	6.7	181	1	RM06_ACACA	P46765 acanthamoeb
43	88	6.7	322	1	GP18_CAEEL	P49048 caenorhabdi
44	88	6.7	377	1	Y835_METJA	O58245 methanococc
45	87.5	6.6	357	1	SP11_RABPU	P42928 rabbitpox v

ALIGNMENTS

RESULT 1
SPEA_STRPY
ID SPEA_STRPY STANDARD; PRT; 251 AA.
AC P08095;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin)
DE (SPE A).
GN SPEA OR SPYM18_0393.
OS Streptococcus pyogenes, and
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314, 186103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86166804; PubMed=3514452;
RA Weeks C.R., Ferretti J.J.;
RT "Nucleotide sequence of the type A streptococcal exotoxin
(erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage
T12";
RT Infect. Immun. 52:144-150(1986).
RL [2]
RN SEQUENCE FROM N.A.
RP MEDLINE=86284313; PubMed=3526093;
RA Johnson L.P., L'Italien J.J., Schlievert P.M.;
RT "Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is
related to Staphylococcus aureus enterotoxin B";
Mol. Gen. Genet. 203:354-356(1986).
RL [3]
RN SEQUENCE FROM N.A.
RP STRAIN=MGAS8232 / Serotype M18;
RX MEDLINE=21927593; PubMed=11917108;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
Syva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
group A Streptococcus strains associated with acute rheumatic fever
outbreaks";
Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
RL [4]
RN X-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).
RX MEDLINE=99094897; PubMed=9878045;
RA Papageorgiou A.C., Collins C.M., Gutman D.M., Kline J.B.,
O'Brien S.M., Tranter H.S., Acharya K.R.;
RT "Structural basis for the recognition of superantigen streptococcal
pyrogenic exotoxin A (SpeA) by MHC class II molecules and T-cell
receptors";
EMBO J. 18:9-21(1999).
RL -|- SUBUNIT: Binds to major histocompatibility complex class II beta
chain.
CC -|- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE
THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET
FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE

QY	15	VLVTEFLGLTIS-QEYFAQDDP--PSQHRSS-LYKNIQNLYFLYEGDPVTHENVK
Db	11	ILIFALIVISPNVLAESQPPMPDDLHKSEFTGTGMNKMKYLDHYVSATKVK
QY	71	LISHLLIYNVSG---PNYDKLKLTKNOEMATLFKDKNDVIYGVVEYHLCYLC--E
Db	71	FLAHLDIYNISDKLKNYDKVKTLLNEDLAKKYADEVDVIGSNYYVNCYFSSKK
QY	126	----SACIYGGVTHNEGHNLEIP--KKIVKSVISDIOGSLSFSDIETNKKMVAQEL
Db	131	VTGGRCTMVGGITKEGHNHFONGNLQNLVRYENKRNITISFEVTDKKSVAQEL
QY	180	RYLTDNKLQNTGSKSYETGYIKFIPKNKESFWDFPEP--EFTOSKYLMIYKDR
Db	191	RNFLKNKNLYEENSPIETGYIKFIENNNGNTFWYDMMPAPGDKFDQSKYLLMYND
QY	238	DSNTSQIEVYLTTK 251
Db	251	DSKSVKIEVHLTTK 264
RESULT 4		
QY	ETC2_STA00	
Db	ID ETC2_STA00	STANDARD; PRT; 266 RA.
QY	AC P34071;	
Db	DT 01-FEB-1994 (Rel. 28, Created)	
QY	DT 01-FEB-1994 (Rel. 28, Last sequence update)	
Db	DT 15-SEP-2003 (Rel. 42, Last annotation update)	
QY	DE Enterotoxin type C-2 precursor (SEC2).	
Db	GN EMTC2.	
QY	OS Staphylococcus aureus.	
Db	OS Bacteria; Firmicutes; Bacillales; Staphylococcus.	
QY	OX NCBI_TaxID=1280;	
Db	EN [1]	
QY	RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-66.	
Db	RX MEDLINE=99277549; PubMed=2543637;	
QY	RA Bohach G.A., Schlievert P.M.;	
Db	RT "Conservation of the biologically active portions of staphylococcal	
QY	RT enterotoxins C1 and C2.";	
Db	RL Infect. Immun. 57:2249-2252(1989).	
QY	EN [2]	
Db	RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).	
QY	RX MEDLINE=96027099; PubMed=7582894;	
Db	RA Papageorgiou A.C., Acharya K.R., Shapiro R., Passalacqua E.F.,	
QY	RT Brehm R.D., Tranter H.S.;	
Db	RT "Crystal structure of the superantigen enterotoxin C2 from	
QY	RL Staphylococcus aureus reveals a zinc-binding site.";	
Db	RN Structure 3:769-779(1995).	
QY	EN [3]	
Db	RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).	
QY	RX MEDLINE=96022987; PubMed=7552730;	
Db	RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;	
QY	RT "Residues defining v beta specificity in staphylococcal	
Db	RT enterotoxins.";	
QY	RL Nat. Struct. Biol. 2:680-686(1995).	
Db	EN [4]	
QY	RP COMPARISON OF STRUCTURE OF SEA AND SEC2.	
Db	RX MEDLINE=97334373; PubMed=9191070;	
QY	RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;	
Db	RT "A structural and functional comparison of staphylococcal	
QY	RT enterotoxins A and C2 reveals remarkable similarity and	
Db	RT dissimilarity.";	
QY	RL J. Mol. Biol. 269:270-280(1997).	
Db	CC -1- COPACITOR: Binds 1 zinc ion per subunit. The zinc ion is necessary	
QY	CC -1- for the toxin interaction with MHC class II.	
Db	CC -1- SURCELLULAR LOCATION: Secreted.	
QY	CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION	
Db	CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.	
QY	CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN	
Db	CC FAMILY.	
QY	PIR: A60114; A60114.	
Db	DR PDB: 1STF. 23-Dec-96	

CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -/- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/
CC STREPTOCOCCAL TOXIN FAMILY.
CC PIR; A60114; A60114. DR
DR PDR; 1 STEF. 22-DEC-05

Query Match 41.3%; Score 547; DB 1; Length 266;
 Best Local Similarity 44.5%; Pred. No. 1.5e-34;
 Matches 114; Conservative 51; Mismatches 73; Indels 18; Gaps 8;

QY 11 MVE-FVLVFLGLTISQEVFAQDDPDPQSLHRSLLVKNL-ONIFYFLYEGDPVTHENVKSV 68
 DB 12 LIPALLILVLPVNLAE---SQDPTPDELHKASKFTGLMKNKVLDDHYVSATKVKSV 68

QY 69 DQLLSHLIYVNSG---PNYDKLTKLQKQEMATLFDKKNVDIYGYEYVHLVCYC--ENA 123
 DB 69 DKFLADLIYINISDKLKNYDKVKTLLNEGLAKKYKDEVDVYGSYNYVNCYFSSKDNV 128

QY 124 ER-----SACIYGGVTNHEGNHLEIP---KKIVKVSIDIGISLFSFIETNKKMVTAGELDY 177
 DB 129 GKVTGKTCMYGGITRHEGNHFDGNLQNVLRVYENKRNITISFEVOTDKSVTAQELDI 188

QY 178 KVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFEPP- EFTOSKYLMIYKDNE 235
 DB 189 KARNFLINKNLKLYEFNSPYETGYIKFIENNGNTFWYDMAPGDKFDQSKYLMIYNDNK 248

QY 236 TLDSTNSQIEVYLTK 251
 DB 249 TVDSKSVKIEVHLTK 264

RESULT 6
 ETXG_STAAU STANDARD; PRT; 258 AA.

AC O85382;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Enterotoxin type G precursor (SEG).
 GN ENTG OR SEG OR SAV1824 OR SAV1642.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OC NCBI_TaxID=158878, 158879, 1280;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN-FR1572;
 RX MEDLINE=98298056; PubMed=9632603;
 RA Munson S.H., Tremaine M.T., Betley M.J., Welch R.A.;
 RT "Identification and Characterization of staphylococcal enterotoxin
 types G and I from Staphylococcus aureus";
 RL Infect. Immun. 66:3337-3348(1998).
 RN [2]

RP SEQUENCE FROM N.A.
 ETXG_STAAU STANDARD; PRT; 258 AA.
 AC MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-U I., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kihara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus";
 RL Lancet 357:1225-1240(2001).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 FAMILY.

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CC EMBL; AF064773; AAC26660.1; -;
 CC DR EMBL; AP003363; BAB57986.1; -;
 DR EMBL; AF003135; BAB42910.1; -;
 DR PIR; G89968; G89968.
 DR HSSP; P01552; LSBB.
 DR InterPro; IPR006177; Bcrlr_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF02876; Staph_strep_tox_C; 1.
 DR Pfam; PF01123; Staph_strep_toxin; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1. Complete proteome.
 KW Enterotoxin; Toxin; Signal; Superantigen;
 FT SIGNAL 1 25 ENTEROTOXIN TYPE G.
 FT CHAIN 26 238 BY SIMILARITY.
 FT DISULFID 116 133
 SQ SEQUENCE 258 AA; 29940 MW; E2982101701D012C CRC64;

Query Match 36.3%; Score 480; DB 1; Length 258;
 Best Local Similarity 40.7%; Pred. No. 1.7e-29;
 Matches 105; Conservative 46; Mismatches 91; Indels 16; Gap

QY 8 LKKMVFVLTFTLGLTISQEVFAQDDPDP--SQLHRSLLVKN---LQNIYFLYEGDPV
 DB 1 MKKLSTVILILILEIVFHNHNVNAQDPKLDLKNKVSIDYKKNKGTGNGVNNLYTSPFP
 QY 62 HENVKSVQDLSHLLIYVNSGPNYDKLTKLQKQEMATLFDKKNVDIYGYEYVHLVCYC
 DB 61 GRGVNSRQFLSHDLIFPIEYKSYNEVKTLENTLANNYKDKKVDIFGVPIYFTCII
 QY 122 NAE-----RSACIYGGVTNHEGNHLEIPKIVKVSIDIGISLFSFIETNKKMVTAG
 DB 121 SEPDINQNFQGCCMYGGLTFNSEN-ERDKLITVQVITIDNRQSLGFTITTNKMMVTCI
 QY 176 DYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWDFEPP- EFTOSKYLMIY
 DB 180 DYKARHLTKERKLYEFDGSAFSGYIKFTEKNTNFSWFDLPKKELVDFVYKFLNLI
 QY 233 DNETLDSNTSQIEVYLTK 250
 DB 240 DNKVDKSIKMEVFLNT 257

RESULT 7
 ETXG_STAAU STANDARD; PRT; 258 AA.
 AC P20723;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Enterotoxin type D precursor (SED).
 GN ENTG.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OC NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89359112; PubMed=2549000;
 RA Bayles K.W., Iandolo J.J.;
 RT "Genetic and molecular analyses of the gene encoding staphylococcal
 enterotoxin D";
 RL J. Bacteriol. 171:4799-4806(1989).
 RN [2]
 RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RC STRAIN-ATCC 23235;
 RX MEDLINE=97157473; PubMed=9003758;
 RA Sundstrom M., Abrahmsen L., Antonsson P., Mehindate K., Mourad W.,
 RA Dohlstien M.;
 RT "The crystal structure of staphylococcal enterotoxin type D reveals

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RT ZN2+-mediated homodimerization.";
RL EMBO J. 15:6832-6840(1996).
CC -1- SUBUNIT: HOMODIMER; ZINC-DEPENDENT.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
CC -----
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CC -----
DR EMBL; M28521; AAB06195.1; -.
DR PIR; A33953; A33953.
DR HSP; P13163; ISXT.
DR InterPro; IPR006177; Bcrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF02876; Staph_Strp_tox_C; 1.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; Zinc.
FT SIGNAL 1 25
FT CHAIN 26 258 ENTEROTOXIN TYPE D.
FT METAL 212 212 ZINC.
FT METAL 250 250 ZINC.
FT METAL 252 252 ZINC.
FT VARIANT 114 114 P->A (IN STRAIN ATCC 23235).
SQ SEQUENCE 258 AA; 29746 MW; 4F7C6A28D42597FD CRC64;
-----
Query Match
Best Local Similarity 26.1%; Score 345; DB 1; Length 258;
Matches 93; Conservative 47; Mismatches 101; Indels 20; Gaps 10;
Oy 8 LKKM-VFVLVTFGLTISQ-EVFAQQDPD---PSQLR-----SSLVKNLQNTYFLYEG 57
Db 1 MKRFNLIALLFTSLVSLPLVKNANENIDSVKEKELHKKSELSSTALNNKHYS--ADK 58
Oy 58 DPVTHENVKVDQLLSHLIYN---VSGPNYDKLTKELKQEMATLEKDKNVDIYGYEY 114
Db 59 NPIIGENKSGDQDLNTLLYKFFDTLINFNSKEMAQHFKSNVDYPIRYS 118
Oy 115 HLCYLCNAERSACIYGVNHEGNHLEIPKKIVVKYSIDGQ-SLSFD-IETNKKMVT 172
Db 119 INCYGE-IDTACTYGVTPHEGNKLEKRIKIPINWINGVQVEVSLDKVQTDKKNVT 177
Oy 173 QELDYKVKYKLTQNKQLYTNGP--SKYETGYIKFIPKNKSFDFPFPEFTQSKYIMI 230
Db 178 QELDAQARRYLQDKLKYNNDTLGGKIQRGKIEFSDSGSKSVYDLEVDKGDFFPEKQLRI 237
Oy 231 YKDNETLDSNTSQIEVLTTK 251
Db 238 YSDNKTLSLSTHLHDIYLYEK 258
-----
RESULT 8
ETXE_STAAU STANDARD; PRT; 257 AA.
AC P12993;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Enterotoxin type E precursor (SEE).
GN ENTE.
OS Staphylococcus aureus.
```


DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
3D-structure; Complete proteome.

FT SIGNAL 1 24
FT CHAIN 25 257 ENTEROTOXIN TYPE A.
FT DISULFID 120 130
FT METAL 211 211 ZINC.
FT METAL 249 249 ZINC.
FT METAL 251 251 ZINC.
FT CONFLICT 242 242 T -> S (IN REF. 3).
FT HELIX 28 31
FT TURN 32 33
FT HELIX 39 41
FT TURN 44 45
FT HELIX 46 55
FT TURN 56 56
FT STRAND 59 65
FT STRAND 69 69
FT TURN 73 74
FT STRAND 75 78
FT TURN 79 80
FT STRAND 90 94
FT HELIX 98 104
FT TURN 105 106
FT STRAND 108 116
FT TURN 118 119
FT TURN 125 126
FT STRAND 128 132
FT STRAND 135 137
FT TURN 139 140
FT STRAND 142 149
FT STRAND 151 155
FT TURN 156 157
FT STRAND 158 160
FT HELIX 164 166
FT STRAND 167 171
FT STRAND 173 175
FT HELIX 176 191
FT TURN 193 194
FT HELIX 197 199
FT TURN 200 200
FT STRAND 205 212
FT STRAND 218 221
FT TURN 222 223
FT HELIX 230 233
FT TURN 234 237
FT TURN 238 239
FT STRAND 242 244
FT STRAND 248 255
SQ SEQUENCE 257 AA; ADEBF5BCA1F14677 CRC64;

Query Match 23.68; Score 312; DB 1; Length 257;
Best Local Similarity 31.38; Pred. No. 9e-17;
Matches 81; Conservative 49; Mismatches 107; Indels 22; Gaps 7;
QY 10 KWFFVLVTFGLTI-----SQEFAQQDDPDSQLHRSLSKLNQNIYFLYEGD 58
DB 2 KKTAFLLLFALTLTSPLVNGSEKSEINEKDLRKSELOQTAL-GNLKQIY--YNE 58
QY 59 PVTHENKVSQDLSSHLLIYN---VSGPNYDKLTELKNQEMATLFKDKNVDIYGVYHH 115
DB 59 KAKTENKESHDQFLQHTILFKGFTDHSWYNDLLVDFDSKDIVDKYKGVLYGAVGY 118
QY 116 LCYLCENAERSACIYGGVTHNEGHNLHLEIPKIVKVSIDGTSQSL--SFDITNKKMVTQ 173
DB 119 QC-AGGPNKTACHYGGVTLHDNNRLTEERKVPINLWLDGKQNTVPLETVKTNKNTVQ 177
QY 174 ELDYKVRKLTNDKQLYTN--PSKYETGYIKETPKNKESPFEDFEPETQSKYLMYI 231
DB 178 ELDIQARYLQEKYNLNSOVDFDKVQGLIVFTSTEPSVNYDLFGAQGOYSNTLLRIY 237
QY 232 KDNETLDSNTSQIEVYLTT 250

Db 238 RDNKTINSENHDIYLT 256

RESULT 10
SPEC_STRPY STANDARD; PRT; 235 AA.
AC P13380;
DT 01-JAN-1990 (Rel. 13, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Exotoxin type C precursor (SPE C).
GN SPEC OR SPY0711.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-52.
RC STRAIN-T18P / MGAS 1585;
RX MEDLINE=88314303; PubMed=3045005;
RA Goshorn S.C., Schlievert P.M.;
RT "Nucleotide sequence of streptococcal pyrogenic exotoxin type C.";
RL Infect. Immun. 56:2518-2520(1988).
RN [2]
RP REVISIONS TO 21-26.
RC STRAIN-T18P / MGAS 1585;
RX MEDLINE=92363541; PubMed=1500157;
RA Kapur V., Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
RT "Molecular population genetic evidence of horizontal spread of two alleles of the pyrogenic exotoxin C gene (speC) among pathogenic clones of Streptococcus pyogenes.";
RL Infect. Immun. 60:3513-3517(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 30-235.
RX MEDLINE=97397352; PubMed=9253413;
RA Roussel A., Anderson B.F., Baker H.M., Fraser J.D., Baker E.N.;
RT "Crystal structure of the streptococcal superantigen SPE-C: dimerization and zinc binding suggest a novel mode of interaction with MHC class II molecules.";
RL Nat. Struct. Biol. 4:635-643(1997).
CC -1- SUBUNIT: Binds to major histocompatibility complex class II beta chain.
CC -1- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC FEVER.
CC -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN FAMILY.
CC -----
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CC -----
DR EMBL; M35514; AAA20717.1; ALT_SEQ.
DR EMBL; M97156; AAB59091.1; -.


```

Db 10 IDKKIYSMITCLSFLLYSNVQANSYNTNRHNLSELYKHDSN---LIEADSIKN-----S 62
Qy 68 VDQLLSHLIYNSGPNYDKLTKELKQEMATLFDKKNVDIYGVVEYHLCYLCENASRS 127
Db 63 PDIVTSHLAYSVDKDN---LSVFFEKDWISOEFKDEVDIYALSQAEVCE-CPGKRYEA 118
Qy 128 CIYGGV--TNHGNHLEIPKIVVKSIDGISOFSDFIENKMWTAQELDYKVRKYLTLD 185
Db 119 --FGGITLTNSEKKEIKVP---VNVMDKSKQOPPMETVNVKPKVTAQEVADIKVKLLIK 172
Qy 186 NKOLYTNPSKYETGYIKFIPKNKSEWFD--FPPEFTQSKVLMYKNETLDSNTSQ 243
Db 173 KYDLYNNREQYKSGTVDLNSGKOIVFDLYVFGNGDF--NSMLKIYSNNERIDSTQFH 230
Qy 244 IEVYLT 249
Db 231 VDVVIS 236

RESULT 12
SPEG STRPY STANDARD; PRT; 234 AA.
AC Q9X5C7:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Exotoxin type G precursor (SPE G).
GN SPEG OR SPY0212.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RN STRAIN=M1.
RC STRAIN=9903428; PubMed=9874566;
RA Proft T., Moffatt S.L., Berkahn C.J., Fraser J.D.;
RT "Identification and characterization of novel superantigens from
RT Streptococcus pyogenes."
RL J. Exp. Med. 189:89-102(1999).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvoarov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RA "Complete genome sequence of an M1 strain of Streptococcus pyogenes."
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
CC -1- SUBUNIT: Binds to major histocompatibility complex class II beta
CC chain.
CC -1- DISEASE: Mitogenic for human peripheral blood lymphocytes.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
CC -----
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CC -----
CC EMBL: AF124499; AAD30988.1; -
CC EMBL: AE006489; AAK33303.1; -
CC HSPS: P13380; IAN8.
CC InterPro: IPR006177; Bctrl_tox.
CC InterPro: IPR006123; Staph/Strep_toxin.
CC InterPro: IPR006126; Staph/Strep_tox.
CC InterPro: IPR006173; Staph_tox_OB.
CC Pfam: PF02876; Staph_Strp_tox_C; 1.
CC Pfam: PF01123; Staph_Strp_toxin; 1.

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DR PRINTS; PR00279; BACTRITOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Toxin; Signal; Complete proteome.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 234 EXOTOXIN TYPE G.
SQ SEQUENCE 234 AA; 27262 MW; 49525C49E4BA2052 CRC64;

Query Match 12.2%; Score 162; DB 1; Length 234;
Best Local Similarity 24.1%; Pred. No. 1.8e-05;
Matches 53; Conservative 42; Mismatches 81; Indels 44; Gaps 10;

Qy 63 ENKVDQLSHHLLIYNVSGPNYDK-----LKTCLKQEMA----- 98
Db 26 ENLKDLKSL--REFAYNITPCDYENVEIAFTVNTSIHNTKQKRSECLLYVDISVSLGIT 83
Qy 99 -TLEKDNVDIYGVVEYHLCYLCENASRSACIYGVVNH--EGNHLEIPKIVVKSIDG 155
Db 84 DQFIKGDKVDVFGLPYFNFSPPYVDN-----IYGGIVKHSNQGK---SLQFVGLNQDG 134
Qy 156 IQSL--SFDIETNKKMVTQAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKNKSEFW 213
Db 135 KEYLPSEAVNRKAKQFTLQEFDFKIRKFLMEKNYIY--DSESRYTSGSLFLATKDSKIYE 193
Qy 214 FDFEPEPE--FTQSKYLMYKNETLDS--NTSQIEVYLT 250
Db 194 VDLFNKDDKLLSRDSFFKRYKDKNFSEIEISHFDIVLKT 233.

RESULT 13
TSST STAAU STANDARD; PRT; 234 AA.
AC P06886;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Toxic shock syndrome toxin-1 precursor (TSST-1).
GN TSST.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=87057222; PubMed=3782090;
RA Blomster-Hautamaa D.A., Kreiswirth B.N., Kornblum J.S., Novick R.P.,
RA Schliefert P.M.;
RT "The nucleotide and partial amino acid sequence of toxic shock
RT syndrome toxin-1."
RL J. Biol. Chem. 261:15783-15786(1986).
RN [2]
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=94150598; PubMed=8107781;
RX Acharya K.R., Passalacqua E.F., Jones E.Y., Harlos K., Stuart D.I.,
RX Brehm R.D., Tranter H.S.;
RA "Structural basis of superantigen action inferred from crystal
RA structure of toxic-shock syndrome toxin-1."
RL Nature 367:94-97(1994).
RN [3]
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=94092653; PubMed=8268150;
RX Prasad G.S., Earhart C.A., Murray D.L., Novick R.P., Schliefert P.M.,
RX Ohlendorf D.H.;
RT "Structure of toxic shock syndrome toxin 1."
RL Biochemistry 32:13761-13766(1993).
RN [4]
RN X-RAY CRYSTALLOGRAPHY (2.07 ANGSTROMS).
RX MEDLINE=96319751; PubMed=8759320;
RX Papageorgiou A.C., Brehm R.D., Leonidas D.D., Tranter H.S.,
RX Acharya K.R.;
RT "The refined crystal structure of toxic shock syndrome toxin-1 at
RT 2.07-A resolution."
RL J. Mol. Biol. 260:553-569(1996).
RN [5]

```

RP X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS).
 RA MEDLINE-97337442; PubMed-9194182;
 RA Prasad G.S., Radhakrishnan R., Mitchell D.T., Earhart C.A.,
 RA Dinges M.M., Cook W.J., Schilvert P.M., Ohlendorf D.H.;
 RT "Refined structures of three crystal forms of toxic shock syndrome
 RT toxin-1 and of a tetramutant with reduced activity.";
 RL protein sci. 6:1220-1227(1997).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF MUTANTS.
 RX MEDLINE-98254504; PubMed-9585531;
 RA Earhart C.A., Mitchell D.T., Murray D.L., Pinheiro D.M., Matsumura M.,
 RA Schlievert P.M., Ohlendorf D.H.;
 RT "Structures of five mutants of toxic shock syndrome toxin-1 with
 RT reduced biological activity.";
 RL Biochemistry 37:7194-7202(1998).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DISEASE: THIS TOXIN IS RESPONSIBLE FOR THE SYMPTOMS OF TOXIC
 CC SHOCK SYNDROME.
 CC -!- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 CC FAMILY.
 CC
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 DR EMBL; J02615; AAA26682.1; .
 DR PIR; A24606; XCSAS1.
 DR PDB; 2TSS; 24-DEC-97.
 DR PDB; 3TSS; 24-DEC-97.
 DR PDB; 4TSS; 24-DEC-97.
 DR PDB; 5TSS; 24-DEC-97.
 DR PDB; 6TSS; 24-DEC-97.
 DR PDB; 7QIL; 12-AUG-97.
 DR PDB; 8QIL; 12-AUG-97.
 DR PDB; 1AW7; 18-NOV-98.
 DR PDB; 1T52; 16-DEC-98.
 DR PDB; 1T53; 16-DEC-98.
 DR PDB; 1T54; 16-DEC-98.
 DR PDB; 1T55; 16-DEC-98.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR InterPro; IPR006125; Staph_toxin.
 DR Pfam; PF02876; Staph_strep_tox_C; 1.
 DR Pfam; PF01123; Staph_strep_toxin; 1.
 DR PRINTS; PR01501; TOXICSTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 DR Toxin; Superantigen; signal; 3D-structure.
 FT SIGNAL 1 40
 FT CHAIN 41 234 TOXIC SHOCK SYNDROME TOXIN-1.
 FT HELIX 46 54
 FT STRAND 58 69
 FT TURN 70 71
 FT STRAND 72 76
 FT TURN 78 79
 FT STRAND 82 86
 FT TURN 90 91
 FT TURN 98 99
 FT STRAND 101 108
 FT STRAND 113 114
 FT TURN 116 117
 FT STRAND 120 125
 FT STRAND 128 129
 FT STRAND 133 138
 FT STRAND 142 146
 FT TURN 147 148
 FT STRAND 149 151
 FT STRAND 159 161
 FT STRAND 163 164

FT HELIX 166 181
 FT TURN 183 185
 FT TURN 187 188
 FT STRAND 192 198
 FT TURN 199 200
 FT STRAND 203 207
 FT TURN 208 209
 FT HELIX 214 216
 FT STRAND 221 222
 FT HELIX 223 225
 FT STRAND 226 234
 SQ SEQUENCE 234 AA; 26306 MW; E95789FF9A1D7AB4 CRC64;
 Query Match. 8.8%; Score 116; DB 1; Length 234;
 Best Local Similarity 23.7%; Pred. No. 0.056;
 Matches 57; Conservative 35; Mismatches 107; Indels 42; Gaps 8;
 QY 4 NKVLKKVFFVLVTLGLTISQEVFAQQDDPPPSOLHRSLSLVK-----NLQNIYELY 55
 DB 2 NKLL--MNFIVSPLLLAATA-----TDFTPVPLSSNQIITAKASTNDIKQLLDWY 53
 QY 56 EGPVTHENVKSVDDLLSHLLIYVSG-----PNYDKLTTELKNEMATLFDKRV 106
 DB 54 SSGSDTFTNSEVLDNSLGSRIKNTDGSISLIIFPSPIYSPAFKGEVDLTKTKRSQ 113
 QY 107 DIYGVYHYHLCYLCAENASACIYGGVTNHEGNHLEIPKIVKVIQSDIGIQS--LSFDIET 165
 DB 114 HTSEGYIHF-----QISGVTNTE--KLPTIELPLKVKVHGKDSPLKYGPKF 159
 QY 166 NKKVWTAQELDYKVKYLTONTKOLYNGSPKYETGYIKFIPKNKESFNFDFPEPEFTQS 225
 DB 160 DKQLAISTLDFEIRHQLTQIHGLYS--SDTGGYWKIWNDSGYIYQSDLSKKEFYNT 217
 QY 226 K 226
 DB 218 K 218
 RESULT 14
 USOL_YEAST STANDARD; PRT; 1790 AA.
 AC P25386;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Intracellular protein transport protein USOL.
 GN USOL OR INT1 OR YDL058W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=X2180-1A;
 RX MEDLINE-91185402; PubMed-2010462;
 RA Nakajima H., Hirata A., Ogawa Y., Yonehara T., Yoda K.,
 RA Yamasaki M.;
 RT "A cytoskeleton-related gene, usol, is required for intracellular
 RT protein transport in Saccharomyces cerevisiae.";
 RL J. Cell Biol. 113:245-260(1991).
 RN [2]
 RP SEQUENCE OF 782-1790 FROM N.A.
 RA Hostetter M.K., Herman D.J., Bendel C.M., McClellan M., Tao N.,
 RA Kendrick K.E.;
 RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 1-8 FROM N.A.
 RA Bai Y., Symington L.S.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: REQUIRED FOR PROTEIN TRANSPORT FROM THE ER TO THE GOLGI
 CC COMPLEX.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC. ASSOCIATED WITH INTRACELLULAR
 CC MEMBRANES. PROBABLY PRESENT ON VESICLES OPERATIONAL BETWEEN THE

```
CC ER AND THE GOLGI COMPLEX.
```

```
CC -1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, COMPOSED
```

```
CC OF AN HEPTAPEPTIDE REPEAT PATTERN CHARACTERISTIC OF ALPHA-HELICAL
```

```
CC COILED COILS. MAY FORM FILAMENTOUS STRUCTURES IN THE CELL.
```

```
CC -1- SIMILARITY: BELONGS TO THE VDP/USOL/YELO47C FAMILY.
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CC -----
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CC -----
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```
CC EMBL; X54378; CAA38253.1; -
```

```
CC DR L03188; AAB00143.1; -
```

```
CC ENBL; U53668; AAB66659.1; -
```

```
CC SGD; S0002216; USOL.
```

```
CC InterPro: IPR002017; Spectrin.
```

```
CC InterPro: IPR006955; Usol_p115.C.
```

```
CC InterPro: IPR006953; Usol_p115_head.
```

```
CC Pfam: PF04871; Usol_p115.C; 1.
```

```
CC Pfam: PF04869; Usol_p115_head; 1.
```

```
CC Transport; Protein transport; Golgi stack; Cytoskeleton; Coiled coil.
```

```
CC KW DOMAIN 1 724 GLOBULAR HEAD.
```

```
CC FT DOMAIN 725 1790 COILED COIL (POTENTIAL).
```

```
CC FT DOMAIN 465 487 CHARGED (HYPER-HYDROPHILIC).
```

```
CC FT DOMAIN 991 1790 DISPENSABLE FOR THE PROTEIN FUNCTION.
```

```
CC FT DOMAIN 1172 1786 ASP/GLU-RICH (ACIDIC).
```

```
CC FT CONFLICT 847 847 G -> E (IN REF. 2).
```

```
CC FT CONFLICT 924 924 E -> K (IN REF. 2).
```

```
CC FT CONFLICT 1253 1253 V -> I (IN REF. 2).
```

```
CC FT CONFLICT 1319 1319 I -> V (IN REF. 2).
```

```
CC FT CONFLICT 1461 1461 N -> S (IN REF. 2).
```

```
CC FT CONFLICT 1581 1581 G -> S (IN REF. 2).
```

```
CC FT CONFLICT 1600 1600 I -> V (IN REF. 2).
```

```
CC FT CONFLICT 1661 1661 R -> S (IN REF. 2).
```

```
CC FT CONFLICT 1772 1772 - D -> DEEDDEE (IN REF. 2).
```

```
CC SQ SEQUENCE 1790 AA; 206424 MW; 6CE2B216E9FD4818 CRC64;
```

```
Query Match 7.7%; Score 102.5; DB 1; Length 1790;
```

```
Best Local Similarity 24.1%; Pred. No. 7;
```

```
Matches 62; Conservative 37; Mismatches 105; Indels 53; Gaps 11;
```

```
QY 1 MENNKVLKAKWFFVLTFLGLTISQEVFAQQDDPSQLHRSSL--VKNLONTLYFLVEGD 58
```

```
: : : : : :
```

```
b 1500 LEKSEMKWKLESTIESNETELKSSMETRKSDKELEQSKSAEDIKNLQH-----EKSD 1555
```

```
: : : : : :
```

```
QY 59 PVT--HENYKSVOLLSHLIYNVSGPNYDKLKTELK-----NOEMATLFKDNVDI 108
```

```
: : : : : :
```

```
Dd 1556 LISRINESEKDIEELKSLRIEAKSQSELETVAQELNNAQEKIRINAEENTVLKSKLEDI.1615
```

```
: : : : : :
```

```
QY 109 YGVEYYHLCYLCENASRSACIVGGVTNHGNHLEIPKKVIKVKSIDIGLSFDIETNKK 168
```

```
: : : : : :
```

```
Dd 1616 ER-----ELKDKQAIE---KSNQEKEKLTLTKLEQLDSTQ-----QKA 1654
```

```
: : : : : :
```

```
QY 169 MYTAQELDLYKVRKYLDNQLTYNGPSKETGYIKPKNKSEFWDFPEPETOSKYL 238
```

```
: : : : : :
```

```
Dd 1655 QXSEERRAVRKFQVEKSQL-DEKAMLETKNVDLV--NKEQAW----KRDEDTVKK-- 1705
```

```
: : : : : :
```

```
QY 229 MIYKONETLDSNTSQTE 245
```

```
: : : : : :
```

```
Dd 1706 -----TTDSQRQEI 1715
```

```
: : : : : :
```

```
RESULT 15
```

```
DSCL_HUMAN STANDARD; PRt; 894 AA.
```

```
ID DSCL_HUMAN
```

```
AC Q08554;
```

```
DT 01-NOV-1997 (Rel. 35, Created)
```

```
DT 01-NOV-1997 (Rel. 35, Last sequence update)
```

```
DT 15-SEP-2003 (Rel. 42, Last annotation update)
```

```
DE Desmocollin IA/IB precursor (Desmosomal glycoprotein 2/3) (DG2/DG3).
```

DR PRINTS; PRO0205; CADHERIN.
DR SMART; SM00112; CA; 5.
DR PROSITE; PS00232; CADHERIN_1; 3.
DR PROSITE; PS02768; CADHERIN_2; 5.
KW Cell adhesion; Glycoprotein; Transmembrane; Repeat; Signal;
KW Cytoskeleton; Calcium-binding; Alternative splicing.
FT SIGNAL 1 29 POTENTIAL.
FT PROPEP 30 134 POTENTIAL.
FT CHAIN 135 894 DESMOCELLIN 1A/1B.
FT DOMAIN 135 691 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 692 714 POTENTIAL.
FT DOMAIN 715 894 POTENTIAL.
FT DOMAIN 135 242 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 243 354 CADHERIN 1.
FT DOMAIN 355 471 CADHERIN 2.
FT DOMAIN 472 575 CADHERIN 3.
FT DOMAIN 576 682 CADHERIN 4.
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 546 546 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 830 840 KVLGCGDEEH -> ESIRGHTLIKN (in isoform 1B).
FT VARSPLIC 841 894 /FTIG-VSP_000651.
FT CONFLICT 132 132 Missing (in isoform 1B)..
FT CONFLICT 132 132 /FTIG-VSP_000652.
SQ SEQUENCE 894 AA; 100044 MW; 44BA33038699E3E1 CRC64;
T -> S (in REF. 3).
Query Match 7.6%; Score 101; DB 1; Length 894;
Best Local Similarity 19.8%; Pred. No. 3.9;
Matches 51; Conservative 43; Mismatches 79; Indels 84; Gaps 10;
QY 34 PPSQLHRSSLVKNLQNIYLYEGDPVTHENKVSQDLSSHLYNVSGPNYDKLTKELK 93
Db 138 PIPASLMENSLGPPQHV-----QQIQS-DAAQNYTIFYSIGPGVDKEPENLF 185
QY 94 NQEMAT--LFKDKNVDIYGYEYHLYCLCENAEARSACIYGGVTNHEGNHLEIPKKIVVKV 151
Db 186 YIEKDTGDICTRSIDREKYEQF-----ALGYATTADGYAPEYPLPLIKI 232
QY 152 SIDGIQSLSFQIE-----TNKRMVTAQELD-----YKVRKYLTDNQ 188
Db 233 EDNDNAPYFEHRYTIFTVPENCSTSGVKVTATDLDEPDLHTLKYKILQIQIPDHPK 292
QY 189 LYTNGPSKYETGYI----KEIPKNKESFW-----FDFF----- 217
Db 293 HFSIHP--DTGVITTTPLDREKCDTYQLIMEVRDMGQPGFLGTITISLEDEND 349
QY 218 PEPEFTQSKYLMYKDN 234
350 NPPSFTETSYTEVEEN 366

Search completed: August 21, 2003, 12:48:09
Job time : 32 secs